

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

**BOX PCT/DO-EO**

Commissioner for Patents  
Washington, D.C. 20231

"Express Mail" mailing label number **EL 823 521 240 US**

I hereby certify that this paper is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" under 37 CFR § 1.10 on the date indicated above and addressed to: Commissioner of Patents, Washington, DC 20231, on July 13, 2001.

  
Colleen Hanagan

**NATIONAL STAGE APPLICATION TRANSMITTAL LETTER**  
**APPLICATION FILING UNDER 35 U.S.C. § 371**

Transmitted herewith for filing is the patent application of:

<b>Inventor(s)/Applicant(s):</b>	<b>Ruelle, Jean-Louis and Thonnard, Joelle</b>
<b>International Application No.:</b>	<b>PCT/EP00/00135</b>
<b>International Published Appln. No.:</b>	<b>WO 00/42191</b>
<b>International Filing Date:</b>	<b>10 January 2000</b>
<b>Priority Filing Dates:</b>	<b>15 January 1999, 28 January 1999, 29 January 1999, 09 February 1999, 10 February 1999, 20 February 1999, 23 February 1999 &amp; 25 February 1999</b>
<b>Thirty Month Date:</b>	<b>15 July 2001</b>
<b>Title:</b>	<b>"NOVEL COMPOUNDS"</b>

1. **THIS NEW APPLICATION IS A NATIONAL STAGE APPLICATION UNDER PCT, CHAPTER II WITH A REQUEST FOR EXAMINATION WITHOUT DELAY TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US).**

- ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. § 371;
- ☐ This is a **SECOND** or subsequent submission of items concerning a filing under 35 U.S.C. § 371.

2. ☒ This is an express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).

3. A proper Demand for International Preliminary Examination was made by the 19<sup>TH</sup> month from the earliest claimed priority date.

4. Enclosed items are required for filing under 37 CFR § 1.53(b) and § 1.494(b) or § 1.495(b):

- ☒ One copy of International Publication No. WO 00/42191
- (a) ☒ is transmitted herewith (**required only if not transmitted by the International Bureau**)
- (b) ☐ has been transmitted by the International Bureau
- (c) ☐ is not required, as the application was filed in the United States Receiving Office (RO/US)

**Fees**

☒ The basic national fee set forth in 37 CFR § 1.482 - International Preliminary Examination Fee not paid to USPTO but International Search Report prepared by the EPO or JPO - **\$860.00**

- ☒ Claims in Excess of 20 (2 @ \$18.00)
- ☐ Independent Claims in Excess of 3 ( @ \$80.00)

5. Further enclosed are:

- ☒ One copy of International Preliminary Examination Report.
- ☒ One copy of International Search Report.
- ☐ One copy of Written Opinion.
- ☐ One copy of PCT Request as filed.
- ☐ One copy of Chapter II Demand as filed.

6. ☐ A translation of the International Application into English (35 U.S.C. § 371(c)(2))

7. ☐ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. § 371(c)(3))

8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. § 371(c)(3))

9. Still additional papers enclosed:

- ☐ Assignment with Assignment Recordation Form Cover Sheet
- ☐ Verification Statement Claiming Small Entity Status
- ☐ Declaration or oath is enclosed executed by the inventor
- ☐ An Information Disclosure Statement under 37 CFR § 1.97 and § 1.98
- ☒ Return Acknowledgment Postcard

10. Nucleotide and/or Amino Acid Sequence Submission (if applicable, all necessary)
- A. Enclosed are:
- (a) ☒ Computer Readable Copy of the Sequence Listing
- (b) ☒ Paper Copy (identical to Computer Readable Copy) of the Sequence Listing
- B. ☐ Enclosed is a paper copy of the Sequence Listing. This paper copy and a Computer Readable Form thereof are identical with the Computer Readable Form in another application of the Applicant which is fully identified as follows:
- U.S. Application No.: @@
- Filed: @@
- Attorney Docket No.: @@
- which is believed to comply with the rules set forth in 37 CFR § 1.821 et. seq. Applicants requests pursuant to 37 CFR § 1.821(e) that this Computer Readable Form be used in the present application. **Please TRANSFER the sequence listing from the parent to this application.**
- C. ☒ Statement under 37 CFR § 1.821(f): **The information recorded in computer readable form is identical to the written Sequence Listing.**
- D. ☐ Statement under 37 CFR § 1.821(g) (required when Sequence Listing not submitted at the time of filing under 35 U.S.C. §111(a)) or 37 CFR §1.821(f) (required when Sequence Listing not submitted at the time of filing under the Patent Cooperation Treaty): **The submission of the Sequence Listing includes no new matter.**
- E. ☒ Amendment: Please enter the Sequence Listing into the application.

11. **Preliminary Amendment**

Prior to calculation of fees, kindly enter:

- ☒ Preliminary Amendment submitted herewith
- ☐ do not enter Preliminary Amendment

09/889283  
JC19 Rec'd PCT/PTO  
PATENT 1 3 JUL 2001  
DOCKET NO. BM45348

12. The correspondence address for this application is the Customer No. provided below:

Insert Bar Code Label Here:



25308

PATENT TRADEMARK OFFICE

13. Fee payment being made at this time is enclosed:

* Basic filing fee (\$860.00)	860.00
* Claims in Excess of 20	36.00
* (2 @ \$18.00)	
Independent Claims in Excess of 3	00.00
( @ \$80.00)	
* Total Fees enclosed:	<u>\$896.00</u>

14. The Commissioner is hereby authorized to charge any fees which may be required, or credit any overpayment to Account No. 50-0258. This letter is filed in duplicate for accounting purposes.

Respectfully submitted,

Eric A. Meade  
Registration No. 42,876  
for  
Allen Bloom  
Registration No. 29,135  
Attorney for Applicant

Date: July 13, 2001

DECHERT  
Princeton Pike Corporate Center  
PO Box 5218  
Princeton, New Jersey 08543-5218  
Allen Bloom (609) 620-3214  
Eric A. Meade (609) 620-3248  
Fax: (609) 620-3259  
Attn : Allen Bloom, Esq.  
(609) 620-3214

International Application No.: PCT/EP00/00135  
Attorney Docket No.: BM45348

09889209/889283  
JC18 Rec'd PCT/PTO 13 JUL 2001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Ruelle et al.  
Serial No.: Unknown  
Filed: Herewith  
For: Novel Compounds

Group Art Unit No.: Unknown  
Examiner: Unknown

#7/a

**PRELIMINARY AMENDMENT**

Sir:

Applicant respectfully requests that this Preliminary Amendment be entered in this case before the calculation of fees and before examination of the subject application.

**In the Claims:**

Please delete the claims of the application as filed in the PCT and substitute therefor:

25. An isolated polypeptide comprising a member selected from the group consisting of
- (a) an amino acid sequence matching one of SEQ ID NOs: 2 (BASB051), 4 (BASB057), 6 (BASB060), 8 (BASB061), 10 (BASB063), 12 (BASB065), 14 (BASB066), or 16 (BASB071);
  - (b) an immunogenic polypeptide comprising a fragment sequence of at least 15 amino acids that matches an aligned contiguous segment of one of SEQ ID NOs: 4, 6, 8, 10, 12, 14, or 16;

wherein the isolated polypeptide, when administered to a subject in a suitable composition which can include an adjuvant, or a suitable carrier coupled to the polypeptide, induces an antibody or T-cell immune response to a polypeptide having the sequence of one of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, or 16.

26. An isolated polynucleotide encoding a polypeptide of Claim 25 or the full complement to the isolated polynucleotide.

27. The isolated polypeptide of claim 25, wherein the polypeptide is according to (a).

28. An isolated polynucleotide encoding a polypeptide of Claim 27 or the full complement to the isolated polynucleotide.

29. The isolated polypeptide of claim 25, wherein the polypeptide is according to (b).
30. An isolated polynucleotide encoding a polypeptide of Claim 29 or the full complement to the isolated polynucleotide.
31. The isolated polypeptide of claim 25, wherein the immunogenic fragment of (b) comprises at least 20 amino acids.
32. The isolated polypeptide of Claim 25 wherein the isolated polypeptide of (a) consists of one of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, and 16.
33. An isolated polynucleotide encoding a polypeptide of Claim 32 or the full complement to the isolated polynucleotide.
34. A process for expressing the polynucleotide of Claim 33 comprising transforming a host cell with an expression vector comprising the polynucleotide and culturing the host cell under conditions sufficient for expression of the polynucleotide.
35. A fusion protein comprising the isolated polypeptide of Claim 25.
36. An isolated polynucleotide comprising the polynucleotide of one of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, or 15.-
37. An isolated polynucleotide segment comprising a polynucleotide sequence or the full complement of the entire length of the polynucleotide sequence, wherein the polynucleotide sequence hybridizes to the full complement of one of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, or 15 minus the complement of any stop codon, wherein the hybridization conditions include incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml denatured, sheared salmon sperm DNA, followed by washing in 0.1x SSC at 65°C; and, wherein the polynucleotide sequence is identical to one of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, or 15 minus any terminal stop codon, except that, over the entire length corresponding to one of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, or 15 minus any terminal stop

International Application No.: PCT/EP00/00135

Attorney Docket No.: BM45348

codon,  $n_n$  nucleotides are substituted, inserted or deleted, wherein  $n_n$  satisfies the following expression

$$n_n \leq x_n - (x_n \bullet y)$$

wherein  $x_n$  is the total number of nucleotides in SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, or 15 minus any terminal stop codon,  $y$  is at least 0.95, and wherein any non-integer product of  $x_n$  and  $y$  is rounded down to the nearest integer before subtracting the product from  $x_n$ ; and wherein the polynucleotide sequence detects *Neisseria meningitidis*.

38. An expression vector comprising the isolated polynucleotide of Claim 26.
39. A host cell transformed with the expression vector of Claim 38.
40. A vaccine comprising the polypeptide of Claim 25 and a pharmaceutically acceptable carrier.
41. The vaccine of Claim 40, wherein the vaccine comprises at least one other *Neisseria meningitidis* antigen.
42. An antibody immunospecific for the polypeptide or immunogenic fragment of Claim 25.
43. A method for inducing an immune response in a mammal comprising administration of the polypeptide of Claim 25.
44. A method of diagnosing a *Neisseria meningitidis* infection, comprising identifying a polypeptide of Claim 25, or an antibody that is immunospecific for the polypeptide, present within a biological sample from an animal suspected of having such an infection.
45. A method for inducing an immune response in a mammal comprising administration of the isolated polynucleotide of Claim 26.

International Application No.: PCT/EP00/00135  
Attorney Docket No.: BM45348

46. A therapeutic composition useful in treating humans with *Neisseria meningitidis* comprising at least one antibody directed against the polypeptide of claim 25 and a suitable pharmaceutical carrier.

### **REMARKS**

#### **Claims**

Claims 1-24 have been canceled without prejudice or disclaimer of the subject matter therein. Applicant reserves the right to prosecute, in one or more patent applications, the canceled claims, the claims as originally filed, and any other claims supported by the specification.

New claims 25-46 have been introduced. No new matter is added.

#### **Support**

Support for the new claims is either obvious, or is as described in the text below. Support for compositions of the isolated polypeptide which include an adjuvant recited in the claims may be found, for example, at page 94, lines 15-16. Support for the hybridization conditions may be found, for example, at page 51, lines 27-30. Support for the recitation of sequence relatedness such as in claim 37 may be found in the specification, for example, at page 97, line 21 through page 98, line 15.



International Application No.: PCT/EP00/00135  
Attorney Docket No.: BM45348

**Closing Remarks**

Allowance of the pending claims is respectfully requested.

Respectfully submitted,



Eric A. Meade  
Registration No. 42,876  
for  
Allen Bloom  
Registration No. 29,135  
Attorney for Applicant

DECHERT PRICE & RHOADS  
Princeton Pike Corporate Center  
PO Box 5218  
Princeton, New Jersey 08543-5218  
Allen Bloom (609) 620-3214  
Eric A. Meade (609) 620-3248  
Fax: (609) 620-3259  
Attn: Allen Bloom, Esq.  
(609) 620-3214

## Novel Compounds

5

### **FIELD OF THE INVENTION**

This invention relates to polynucleotides, (herein referred to as "BASB051 polynucleotide(s)", "BASB057 polynucleotide(s)", "BASB060 polynucleotide(s)", "BASB061 polynucleotide(s)", "BASB063 polynucleotide(s)", "BASB065 polynucleotide(s)", "BASB066 polynucleotide(s)" and "BASB071 polynucleotide(s)"), polypeptides encoded by them (referred to herein as "BASB051", "BASB057", "BASB060", "BASB061", "BASB063", "BASB065", "BASB066" and "BASB071" respectively or "BASB051 polypeptide(s)", "BASB057 polypeptide(s)", "BASB060 polypeptide(s)", "BASB061 polypeptide(s)", "BASB063 polypeptide(s)", "BASB065 polypeptide(s)", "BASB066 polypeptide(s)" and "BASB071 polypeptide(s)" respectively), recombinant materials and methods for their production. In another aspect, the invention relates to methods for using such polypeptides and polynucleotides, including vaccines against bacterial infections. In a further aspect, the invention relates to diagnostic assays for detecting infection of certain pathogens.

20

### **BACKGROUND OF THE INVENTION**

*Neisseria meningitidis* (meningococcus) is a Gram-negative bacterium frequently isolated from the human upper respiratory tract. It occasionally causes invasive bacterial diseases such as bacteremia and meningitis. The incidence of meningococcal disease shows geographical seasonal and annual differences (Schwartz, B., Moore, P.S., Broome, C.V.; Clin. Microbiol. Rev. 2 (Supplement), S18-S24, 1989). Most disease in temperate countries is due to strains of serogroup B and varies in incidence from 1-10/100,000/year total population sometimes reaching higher values (Kaczmarek, E.B. (1997), Commun. Dis. Rep. Rev. 7: R55-9, 1995; Scholten, R.J.P.M., Bijlmer, H.A., Poolman, J.T. et al. Clin. Infect. Dis. 16: 237-246, 1993; Cruz, C., Pavez, G., Aguilar, E., et al. Epidemiol. Infect. 105: 119-126, 1990).

30

Epidemics dominated by serogroup A meningococci, mostly in central Africa, are encountered, sometimes reaching levels up to 1000/100.000/year (Schwartz, B., Moore, P.S., Broome, C.V. Clin. Microbiol. Rev. 2 (Supplement), S18-S24, 1989). Nearly all cases as a whole of meningococcal disease are caused by serogroup A, B, C, W-135 and Y meningococci and a tetravalent A, C, W-135, Y polysaccharide vaccine is available (Armand, J., Arminjon, F., Mynard, M.C., Lafaix, C., J. Biol. Stand. 10: 335-339, 1982).

The polysaccharide vaccines are currently being improved by way of chemical conjugating them to carrier proteins (Lieberman, J.M., Chiu, S.S., Wong, V.K., et al. JAMA 275 : 1499-1503, 1996).

A serogroup B vaccine is not available, since the B capsular polysaccharide was found to be nonimmunogenic, most likely because it shares structural similarity to host components (Wyle, F.A., Artenstein, M.S., Brandt, M.L. et al. J. Infect. Dis. 126: 514-522, 1972; Finne, J.M., Leinonen, M., Mäkelä, P.M. Lancet ii.: 355-357, 1983).

For many years efforts have been initiated and carried out to develop meningococcal outer membrane based vaccines (de Moraes, J.C., Perkins, B., Camargo, M.C. et al. Lancet 340: 1074-1078, 1992; Bjune, G., Hoiby, E.A. Gronnesby, J.K. et al. 338: 1093-1096, 1991). Such vaccines have demonstrated efficacies from 57% - 85% in older children (>4 years) and adolescents.

Many bacterial outer membrane components are present in these vaccines, such as PorA, PorB, Rmp, Opc, Opa, FrpB and the contribution of these components to the observed protection still needs further definition. Other bacterial outer membrane components have been defined by using animal or human antibodies to be potentially relevant to the induction of protective immunity, such as TbpB and NspA (Martin, D., Cadieux, N., Hamel, J., Brodeux, B.R., J. Exp. Med. 185: 1173-1183, 1997; Lissolo, L., Maître-Wilmotte, C., Dumas, p. et al.,

Inf. Immun. 63: 884-890, 1995). The mechanisms of protective immunity will involve antibody mediated bactericidal activity and opsonophagocytosis.

A bacteremia animal model has been used to combine all antibody mediated mechanisms (Saukkonen, K., Leinonen, M., Abdillahi, H. Poolman, J. T. Vaccine 7: 325-328, 1989). It is generally accepted that the late complement component mediated bactericidal mechanism is crucial for immunity against meningococcal disease (Ross, S.C., Rosenthal P.J., Berberic, H.M., Densen, P. J. Infect. Dis. 155: 1266-1275, 1987).

10 The frequency of *Neisseria meningitidis* infections has risen dramatically in the past few decades. This has been attributed to the emergence of multiply antibiotic resistant strains and an increasing population of people with weakened immune systems. It is no longer uncommon to isolate *Neisseria meningitidis* strains that are resistant to some or all of the standard antibiotics. This phenomenon has created an unmet medical need and demand for  
15 new anti-microbial agents, vaccines, drug screening methods, and diagnostic tests for this organism.

# **SUMMARY OF THE INVENTION**

20 The present invention relates to BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066, and BASB071, in particular BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066, and BASB071 polypeptides and BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066, and BASB071  
25 polynucleotides, recombinant materials and methods for their production. In another aspect, the invention relates to methods for using such polypeptides and polynucleotides, including prevention and treatment of microbial diseases, amongst others. In a further aspect, the invention relates to diagnostic assays for detecting diseases associated with microbial infections and conditions associated with such infections, such as assays for detecting expression or activity of BASB051, BASB057, BASB060, BASB061, BASB063,  
30 BASB065, BASB066, and BASB071 polynucleotides or polypeptides.

Various changes and modifications within the spirit and scope of the disclosed invention will become readily apparent to those skilled in the art from reading the following descriptions and from reading the other parts of the present disclosure.

5

## DESCRIPTION OF THE INVENTION

The invention relates to BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066, and BASB071 polypeptides and polynucleotides as described in greater detail  
10 below. The invention relates especially to BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066, and BASB071 having the nucleotide and amino acid sequences set out in SEQ ID NO:1,3,5,7,9,11,13,15 and SEQ ID NO:2,4,6,8,10,12,14,16 respectively. It is understood that sequences recited in the Sequence Listing below as “DNA” represent an exemplification of one embodiment of the invention, since those of  
15 ordinary skill will recognize that such sequences can be usefully employed in polynucleotides in general, including ribopolynucleotides.

### Polypeptides

In one aspect of the invention there are provided polypeptides of *Neisseria meningitidis*  
20 referred to herein as “BASB051”, “BASB057”, “BASB060”, “BASB061”, “BASB063”, “BASB065”, “BASB066” and “BASB071”, and “BASB051 polypeptides”, “BASB057 polypeptides”, “BASB060 polypeptides”, “BASB061 polypeptides”, “BASB063 polypeptides”, “BASB065 polypeptides”, “BASB066 polypeptides”, and “BASB071 polypeptides” as well as biologically, diagnostically, prophylactically, clinically or  
25 therapeutically useful variants thereof, and compositions comprising the same.

The present invention further provides for:

(a) an isolated polypeptide which comprises an amino acid sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% or exact identity, to that of SEQ ID NO:2.

(b) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO:1 over the entire length of SEQ ID NO:1.

(c) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity, to the amino acid sequence of SEQ ID NO:2.

The BASB051 polypeptide provided in SEQ ID NO:2 is the BASB051 polypeptide from *Neisseria meningitidis* strain ATCC13090.

15

The invention also provides an immunogenic fragment of a BASB051 polypeptide, that is, a contiguous portion of the BASB051 polypeptide which has the same or substantially the same immunogenic activity as the polypeptide comprising the amino acid sequence of SEQ ID NO:2. That is to say, the fragment (if necessary when coupled to a carrier) is capable of raising an immune response which recognises the BASB051 polypeptide. Such an immunogenic fragment may include, for example, the BASB051 polypeptide lacking an N-terminal leader sequence, and/or a transmembrane domain and/or a C-terminal anchor domain. In a preferred aspect the immunogenic fragment of BASB051 according to the invention comprises substantially all of the extracellular domain of a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to that of SEQ ID NO:2 over the entire length of SEQ ID NO:2.

25

The present invention further provides for:

(a) an isolated polypeptide which comprises an amino acid sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% or exact identity, to that of SEQ ID NO:4.

(b) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO:3 over the entire length of SEQ ID NO:3.

(c) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity, to the amino acid sequence of SEQ ID NO:4

The BASB057 polypeptide provided in SEQ ID NO:4 is the BASB057 polypeptide from *Neisseria meningitidis* strain ATCC13090.

15

The invention also provides an immunogenic fragment of a BASB057 polypeptide, that is, a contiguous portion of the BASB057 polypeptide which has the same or substantially the same immunogenic activity as the polypeptide comprising the amino acid sequence of SEQ ID NO:4. That is to say, the fragment (if necessary when coupled to a carrier) is capable of raising an immune response which recognises the BASB057 polypeptide. Such an immunogenic fragment may include, for example, the BASB057 polypeptide lacking an N-terminal leader sequence, and/or a transmembrane domain and/or a C-terminal anchor domain. In a preferred aspect the immunogenic fragment of BASB057 according to the invention comprises substantially all of the extracellular domain of a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to that of SEQ ID NO:4 over the entire length of SEQ ID NO:4.

20

25

The present invention further provides for:

(a) an isolated polypeptide which comprises an amino acid sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% or exact identity, to that of SEQ ID NO:6.

(b) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO:5 over the entire length of SEQ ID NO:5.

(c) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity, to the amino acid sequence of SEQ ID NO:6

The BASB060 polypeptide provided in SEQ ID NO:6 is the BASB060 polypeptide from *Neisseria meningitidis* strain ATCC13090.

15

The invention also provides an immunogenic fragment of a BASB060 polypeptide, that is, a contiguous portion of the BASB060 polypeptide which has the same or substantially the same immunogenic activity as the polypeptide comprising the amino acid sequence of SEQ ID NO:6. That is to say, the fragment (if necessary when coupled to a carrier) is capable of raising an immune response which recognises the BASB060 polypeptide. Such an immunogenic fragment may include, for example, the BASB060 polypeptide lacking an N-terminal leader sequence, and/or a transmembrane domain and/or a C-terminal anchor domain. In a preferred aspect the immunogenic fragment of BASB060 according to the invention comprises substantially all of the extracellular domain of a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to that of SEQ ID NO:6 over the entire length of SEQ ID NO:6.

25

The present invention further provides for:



(a) an isolated polypeptide which comprises an amino acid sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% or exact identity, to that of SEQ ID NO:8.

(b) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO:7 over the entire length of SEQ ID NO:7.

(c) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity, to the amino acid sequence of SEQ ID NO:8

The BASB061 polypeptide provided in SEQ ID NO:8 is the BASB061 polypeptide from *Neisseria meningitidis* strain ATCC13090.

15

The invention also provides an immunogenic fragment of a BASB061 polypeptide, that is, a contiguous portion of the BASB061 polypeptide which has the same or substantially the same immunogenic activity as the polypeptide comprising the amino acid sequence of SEQ ID NO:8. That is to say, the fragment (if necessary when coupled to a carrier) is capable of raising an immune response which recognises the BASB061 polypeptide. Such an immunogenic fragment may include, for example, the BASB061 polypeptide lacking an N-terminal leader sequence, and/or a transmembrane domain and/or a C-terminal anchor domain. In a preferred aspect the immunogenic fragment of BASB061 according to the invention comprises substantially all of the extracellular domain of a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to that of SEQ ID NO:8 over the entire length of SEQ ID NO:8.

20

25

The present invention further provides for:

(a) an isolated polypeptide which comprises an amino acid sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% or exact identity, to that of SEQ ID NO:10.

(b) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide  
5 sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO:9 over the entire length of SEQ ID NO:9.

(c) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide  
10 sequence encoding a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity, to the amino acid sequence of SEQ ID NO:10

The BASB063 polypeptide provided in SEQ ID NO:10 is the BASB063 polypeptide from *Neisseria meningitidis* strain ATCC13090.

15

The invention also provides an immunogenic fragment of a BASB063 polypeptide, that is, a contiguous portion of the BASB063 polypeptide which has the same or substantially the same immunogenic activity as the polypeptide comprising the amino acid sequence of SEQ ID NO:10. That is to say, the fragment (if necessary when coupled to a carrier) is capable  
20 of raising an immune response which recognises the BASB063 polypeptide. Such an immunogenic fragment may include, for example, the BASB063 polypeptide lacking an N-terminal leader sequence, and/or a transmembrane domain and/or a C-terminal anchor domain. In a preferred aspect the immunogenic fragment of BASB063 according to the invention comprises substantially all of the extracellular domain of a polypeptide which has  
25 at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to that of SEQ ID NO:10 over the entire length of SEQ ID NO:10.

The present invention further provides for:

(a) an isolated polypeptide which comprises an amino acid sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% or exact identity, to that of SEQ ID NO:12.

(b) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO:11 over the entire length of SEQ ID NO:11.

(c) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity, to the amino acid sequence of SEQ ID NO:12

The BASB065 polypeptide provided in SEQ ID NO:12 is the BASB065 polypeptide from *Neisseria meningitidis* strain ATCC13090.

The invention also provides an immunogenic fragment of a BASB065 polypeptide, that is, a contiguous portion of the BASB065 polypeptide which has the same or substantially the same immunogenic activity as the polypeptide comprising the amino acid sequence of SEQ ID NO:12. That is to say, the fragment (if necessary when coupled to a carrier) is capable of raising an immune response which recognises the BASB065 polypeptide. Such an immunogenic fragment may include, for example, the BASB065 polypeptide lacking an N-terminal leader sequence, and/or a transmembrane domain and/or a C-terminal anchor domain. In a preferred aspect the immunogenic fragment of BASB065 according to the invention comprises substantially all of the extracellular domain of a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to that of SEQ ID NO:12 over the entire length of SEQ ID NO:12.

The present invention further provides for:

(a) an isolated polypeptide which comprises an amino acid sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% or exact identity, to that of SEQ ID NO:14.

(b) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO:13 over the entire length of SEQ ID NO:13.

(c) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity, to the amino acid sequence of SEQ ID NO:14

The BASB066 polypeptide provided in SEQ ID NO:14 is the BASB066 polypeptide from *Neisseria meningitidis* strain ATCC13090.

The invention also provides an immunogenic fragment of a BASB066 polypeptide, that is, a contiguous portion of the BASB066 polypeptide which has the same or substantially the same immunogenic activity as the polypeptide comprising the amino acid sequence of SEQ ID NO:14. That is to say, the fragment (if necessary when coupled to a carrier) is capable of raising an immune response which recognises the BASB066 polypeptide. Such an immunogenic fragment may include, for example, the BASB066 polypeptide lacking an N-terminal leader sequence, and/or a transmembrane domain and/or a C-terminal anchor domain. In a preferred aspect the immunogenic fragment of BASB066 according to the invention comprises substantially all of the extracellular domain of a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% identity, to that of SEQ ID NO:14 over the entire length of SEQ ID NO:14.

The present invention further provides for:





The polypeptides, or immunogenic fragments, of the invention may be in the form of the "mature" protein or may be a part of a larger protein such as a precursor or a fusion protein. It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in

5 purification such as multiple histidine residues, or an additional sequence for stability during recombinant production. Furthermore, addition of exogenous polypeptide or lipid tail or polynucleotide sequences to increase the immunogenic potential of the final molecule is also considered.

10 In one aspect, the invention relates to genetically engineered soluble fusion proteins comprising a polypeptide of the present invention, or a fragment thereof, and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE). Preferred as an immunoglobulin is the constant part of the heavy chain of human IgG, particularly IgG1, where fusion takes place at the hinge

15 region. In a particular embodiment, the Fc part can be removed simply by incorporation of a cleavage sequence which can be cleaved with blood clotting factor Xa.

Furthermore, this invention relates to processes for the preparation of these fusion proteins by genetic engineering, and to the use thereof for drug screening, diagnosis and

20 therapy. A further aspect of the invention also relates to polynucleotides encoding such fusion proteins. Examples of fusion protein technology can be found in International Patent Application Nos. WO94/29458 and WO94/22914.

The proteins may be chemically conjugated, or expressed as recombinant fusion proteins

25 allowing increased levels to be produced in an expression system as compared to non-fused protein. The fusion partner may assist in providing T helper epitopes (immunological fusion partner), preferably T helper epitopes recognised by humans, or assist in expressing the protein (expression enhancer) at higher yields than the native recombinant protein. Preferably the fusion partner will be both an immunological fusion

30 partner and expression enhancing partner.





A polypeptide of the invention may also be obtained, for example, from organisms of the same taxonomic family or order.

### **Polynucleotides**

- 5 It is an object of the invention to provide polynucleotides that encode BASB051 polypeptides, particularly polynucleotides that encode the polypeptide herein designated BASB051.

- 10 In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding BASB051 polypeptides comprising a sequence set out in SEQ ID NO:1 which includes a full length gene, or a variant thereof.

The BASB051 polynucleotide provided in SEQ ID NO:1 is the BASB051 polynucleotide from *Neisseria meningitidis* strains ATCC13090.

15

- As a further aspect of the invention there are provided isolated nucleic acid molecules encoding and/or expressing BASB051 polypeptides and polynucleotides, particularly *Neisseria meningitidis* BASB051 polypeptides and polynucleotides, including, for example, unprocessed RNAs, ribozyme RNAs, mRNAs, cDNAs, genomic DNAs, B- and  
20 Z-DNAs. Further embodiments of the invention include biologically, diagnostically, prophylactically, clinically or therapeutically useful polynucleotides and polypeptides, and variants thereof, and compositions comprising the same.

- Another aspect of the invention relates to isolated polynucleotides, including at least one full  
25 length gene, that encodes a BASB051 polypeptide having a deduced amino acid sequence of SEQ ID NO:2 and polynucleotides closely related thereto and variants thereof.

- In another particularly preferred embodiment of the invention there is a BASB051 polypeptide from *Neisseria meningitidis* comprising or consisting of an amino acid  
30 sequence of SEQ ID NO:2 or a variant thereof.

Using the information provided herein, such as a polynucleotide sequence set out in SEQ ID NO:1 a polynucleotide of the invention encoding BASB051 polypeptide may be obtained using standard cloning and screening methods, such as those for cloning and sequencing chromosomal DNA fragments from bacteria using *Neisseria meningitidis* cells as starting material, followed by obtaining a full length clone. For example, to obtain a polynucleotide sequence of the invention, such as a polynucleotide sequence given in SEQ ID NO:1 typically a library of clones of chromosomal DNA of *Neisseria meningitidis* in *E. coli* or some other suitable host is probed with a radiolabeled oligonucleotide, preferably a 17-mer or longer, derived from a partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using stringent hybridization conditions. By sequencing the individual clones thus identified by hybridization with sequencing primers designed from the original polypeptide or polynucleotide sequence it is then possible to extend the polynucleotide sequence in both directions to determine a full length gene sequence. Conveniently, such sequencing is performed, for example, using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL*, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989). (see in particular Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70). Direct genomic DNA sequencing may also be performed to obtain a full length gene sequence. Illustrative of the invention, each polynucleotide set out in SEQ ID NO:1 was discovered in a DNA library derived from *Neisseria meningitidis*.

Moreover, the DNA sequence set out in SEQ ID NO:1 contains an open reading frame  
25 encoding a protein having about the number of amino acid residues set forth in SEQ ID NO:2  
with a deduced molecular weight that can be calculated using amino acid residue molecular  
weight values well known to those skilled in the art.



rho-dependent and rho-independent termination signals), ribosome binding sites, Kozak sequences, sequences that stabilize mRNA, introns, and polyadenylation signals. The polynucleotide sequence may also comprise additional coding sequence encoding additional amino acids. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain embodiments of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al.*, *Proc. Natl. Acad. Sci., USA* 86: 821-824 (1989), or an HA peptide tag (Wilson *et al.*, *Cell* 37: 767 (1984), both of which may be useful in purifying polypeptide sequence fused to them. Polynucleotides of the invention also include, but are not limited to, polynucleotides comprising a structural gene and its naturally associated sequences that control gene expression.

The nucleotide sequence encoding BASB051 polypeptide of SEQ ID NO:2 may be identical to the polypeptide encoding sequence contained in nucleotides 1 to 801 of SEQ ID NO:1. Alternatively it may be a sequence, which as a result of the redundancy (degeneracy) of the genetic code, also encodes the polypeptide of SEQ ID NO:2.

The term "polynucleotide encoding a polypeptide" as used herein encompasses polynucleotides that include a sequence encoding a polypeptide of the invention, particularly a bacterial polypeptide and more particularly a polypeptide of the *Neisseria meningitidis* BASB051 having an amino acid sequence set out in SEQ ID NO:2. The term also encompasses polynucleotides that include a single continuous region or discontinuous regions encoding the polypeptide (for example, polynucleotides interrupted by integrated phage, an integrated insertion sequence, an integrated vector sequence, an integrated transposon sequence, or due to RNA editing or genomic DNA reorganization) together with additional regions, that also may contain coding and/or non-coding sequences.

The invention further relates to variants of the polynucleotides described herein that encode variants of a polypeptide having a deduced amino acid sequence of SEQ ID NO:2.

Fragments of polynucleotides of the invention may be used, for example, to synthesize full-length polynucleotides of the invention.



hybridization occurring only if there is at least 95% and preferably at least 97% identity between the sequences. A specific example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 5 10% dextran sulfate, and 20 micrograms/ml of denatured, sheared salmon sperm DNA, followed by washing the hybridization support in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein. Solution hybridization may also be used with the 10 polynucleotide sequences provided by the invention.

The invention also provides a polynucleotide consisting of or comprising a polynucleotide sequence obtained by screening an appropriate library containing the complete gene for a polynucleotide sequence set forth in SEQ ID NO:1 under stringent hybridization conditions 15 with a probe having the sequence of said polynucleotide sequence set forth in SEQ ID NO:1 or a fragment thereof; and isolating said polynucleotide sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers fully described elsewhere herein.

20 As discussed elsewhere herein regarding polynucleotide assays of the invention, for instance, the polynucleotides of the invention, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding BASB051 and to isolate cDNA and genomic clones of other genes that have a high identity, particularly high sequence identity, to the BASB051 gene. Such probes generally will comprise at least 15 25 nucleotide residues or base pairs. Preferably, such probes will have at least 30 nucleotide residues or base pairs and may have at least 50 nucleotide residues or base pairs. Particularly preferred probes will have at least 20 nucleotide residues or base pairs and will have less than 30 nucleotide residues or base pairs.

A coding region of a BASB051 gene may be isolated by screening using a DNA sequence provided in SEQ ID NO:1 to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine which members of the library the  
5 probe hybridizes to.

It is an object of the invention to provide polynucleotides that encode BASB057 polypeptides, particularly polynucleotides that encode the polypeptide herein designated BASB057.

- 5 In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding BASB057 polypeptides comprising a sequence set out in SEQ ID NO:3 which includes a full length gene, or a variant thereof.

The BASB057 polynucleotide provided in SEQ ID NO:3 is the BASB057 polynucleotide  
10 from *Neisseria meningitidis* strains ATCC13090.

As a further aspect of the invention there are provided isolated nucleic acid molecules encoding and/or expressing BASB057 polypeptides and polynucleotides, particularly *Neisseria meningitidis* BASB057 polypeptides and polynucleotides, including, for  
15 example, unprocessed RNAs, ribozyme RNAs, mRNAs, cDNAs, genomic DNAs, B- and Z-DNAs. Further embodiments of the invention include biologically, diagnostically, prophylactically, clinically or therapeutically useful polynucleotides and polypeptides, and variants thereof, and compositions comprising the same.

- 20 Another aspect of the invention relates to isolated polynucleotides, including at least one full length gene, that encodes a BASB057 polypeptide having a deduced amino acid sequence of SEQ ID NO:4 and polynucleotides closely related thereto and variants thereof.

In another particularly preferred embodiment of the invention there is a BASB057  
25 polypeptide from *Neisseria meningitidis* comprising or consisting of an amino acid sequence of SEQ ID NO:4 or a variant thereof.

Using the information provided herein, such as a polynucleotide sequence set out in SEQ ID NO:3 a polynucleotide of the invention encoding BASB057 polypeptide may be obtained  
30 using standard cloning and screening methods, such as those for cloning and sequencing



chromosomal DNA fragments from bacteria using *Neisseria meningitidis* cells as starting material, followed by obtaining a full length clone. For example, to obtain a polynucleotide sequence of the invention, such as a polynucleotide sequence given in SEQ ID NO:3

typically a library of clones of chromosomal DNA of *Neisseria meningitidis* in *E.coli* or

5 some other suitable host is probed with a radiolabeled oligonucleotide, preferably a 17-mer or longer, derived from a partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using stringent hybridization conditions. By sequencing the individual clones thus identified by hybridization with sequencing primers designed from the original polypeptide or polynucleotide sequence it is then possible to extend the

10 polynucleotide sequence in both directions to determine a full length gene sequence. Conveniently, such sequencing is performed, for example, using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL*, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989). (see

15 in particular Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70). Direct genomic DNA sequencing may also be performed to obtain a full length gene sequence. Illustrative of the invention, each polynucleotide set out in SEQ ID NO:3 was discovered in a DNA library derived from *Neisseria meningitidis*.

20 Moreover, the DNA sequence set out in SEQ ID NO:3 contains an open reading frame encoding a protein having about the number of amino acid residues set forth in SEQ ID NO:4 with a deduced molecular weight that can be calculated using amino acid residue molecular weight values well known to those skilled in the art.

25 The polynucleotide of SEQ ID NO:3, between the start codon at nucleotide number 1 and the stop codon which begins at nucleotide number 1402 of SEQ ID NO:3, encodes the polypeptide of SEQ ID NO:4.

In a further aspect, the present invention provides for an isolated polynucleotide comprising  
30 or consisting of:



*et al.*, *Proc. Natl. Acad. Sci., USA* 86: 821-824 (1989), or an HA peptide tag (*Wilson et al.*, *Cell* 37: 767 (1984), both of which may be useful in purifying polypeptide sequence fused to them. Polynucleotides of the invention also include, but are not limited to, polynucleotides comprising a structural gene and its naturally associated sequences that control gene expression.

The nucleotide sequence encoding BASB057 polypeptide of SEQ ID NO:4 may be identical to the polypeptide encoding sequence contained in nucleotides 1 to 1401 of SEQ ID NO:3. Alternatively it may be a sequence, which as a result of the redundancy (degeneracy) of the genetic code, also encodes the polypeptide of SEQ ID NO:4.

The term "polynucleotide encoding a polypeptide" as used herein encompasses polynucleotides that include a sequence encoding a polypeptide of the invention, particularly a bacterial polypeptide and more particularly a polypeptide of the *Neisseria meningitidis* BASB057 having an amino acid sequence set out in SEQ ID NO:4. The term also encompasses polynucleotides that include a single continuous region or discontinuous regions encoding the polypeptide (for example, polynucleotides interrupted by integrated phage, an integrated insertion sequence, an integrated vector sequence, an integrated transposon sequence, or due to RNA editing or genomic DNA reorganization) together with additional regions, that also may contain coding and/or non-coding sequences.

The invention further relates to variants of the polynucleotides described herein that encode variants of a polypeptide having a deduced amino acid sequence of SEQ ID NO:4.

Fragments of polynucleotides of the invention may be used, for example, to synthesize full-length polynucleotides of the invention.

Further particularly preferred embodiments are polynucleotides encoding BASB057 variants, that have the amino acid sequence of BASB057 polypeptide of SEQ ID NO:4 in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, modified, deleted and/or added, in any combination. Especially preferred among these are silent

substitutions, additions and deletions, that do not alter the properties and activities of BASB057 polypeptide.

Further preferred embodiments of the invention are polynucleotides that are at least 85% identical over their entire length to a polynucleotide encoding BASB057 polypeptide having an amino acid sequence set out in SEQ ID NO:4 and polynucleotides that are complementary to such polynucleotides. In this regard, polynucleotides at least 90% identical over their entire length to the same are particularly preferred, and among these particularly preferred polynucleotides, those with at least 95% are especially preferred. Furthermore, those with at least 97% are highly preferred among those with at least 95%, and among these those with at least 98% and at least 99% are particularly highly preferred, with at least 99% being the more preferred.

Preferred embodiments are polynucleotides encoding polypeptides that retain substantially  
15 the same biological function or activity as the mature polypeptide encoded by a DNA of SEQ  
ID NO:3.

In accordance with certain preferred embodiments of this invention there are provided polynucleotides that hybridize, particularly under stringent conditions, to BASB057  
20 polynucleotide sequences, such as those polynucleotides in SEQ ID NO:3.

The invention further relates to polynucleotides that hybridize to the polynucleotide sequences provided herein. In this regard, the invention especially relates to polynucleotides that hybridize under stringent conditions to the polynucleotides described herein. As herein  
25 used, the terms "stringent conditions" and "stringent hybridization conditions" mean hybridization occurring only if there is at least 95% and preferably at least 97% identity between the sequences. A specific example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution.  
30 10% dextran sulfate, and 20 micrograms/ml of denatured, sheared salmon sperm DNA,



It is an object of the invention to provide polynucleotides that encode BASB060 polypeptides, particularly polynucleotides that encode the polypeptide herein designated BASB060.

- 5 In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding BASB060 polypeptides comprising a sequence set out in SEQ ID NO:5 which includes a full length gene, or a variant thereof.

The BASB060 polynucleotide provided in SEQ ID NO:5 is the BASB060 polynucleotide  
10 from *Neisseria meningitidis* strains ATCC13090.

As a further aspect of the invention there are provided isolated nucleic acid molecules encoding and/or expressing BASB060 polypeptides and polynucleotides, particularly *Neisseria meningitidis* BASB060 polypeptides and polynucleotides, including, for  
15 example, unprocessed RNAs, ribozyme RNAs, mRNAs, cDNAs, genomic DNAs, B- and Z-DNAs. Further embodiments of the invention include biologically, diagnostically, prophylactically, clinically or therapeutically useful polynucleotides and polypeptides, and variants thereof, and compositions comprising the same.

20 Another aspect of the invention relates to isolated polynucleotides, including at least one full length gene, that encodes a BASB060 polypeptide having a deduced amino acid sequence of SEQ ID NO:6 and polynucleotides closely related thereto and variants thereof.

In another particularly preferred embodiment of the invention there is a BASB060  
25 polypeptide from *Neisseria meningitidis* comprising or consisting of an amino acid sequence of SEQ ID NO:6 or a variant thereof.

Using the information provided herein, such as a polynucleotide sequence set out in SEQ ID NO:5 a polynucleotide of the invention encoding BASB060 polypeptide may be obtained  
30 using standard cloning and screening methods, such as those for cloning and sequencing

chromosomal DNA fragments from bacteria using *Neisseria meningitidis* cells as starting material, followed by obtaining a full length clone. For example, to obtain a polynucleotide sequence of the invention, such as a polynucleotide sequence given in SEQ ID NO:5 typically a library of clones of chromosomal DNA of *Neisseria meningitidis* in *E.coli* or  
5 some other suitable host is probed with a radiolabeled oligonucleotide, preferably a 17-mer or longer, derived from a partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using stringent hybridization conditions. By sequencing the individual clones thus identified by hybridization with sequencing primers designed from the original polypeptide or polynucleotide sequence it is then possible to extend the  
10 polynucleotide sequence in both directions to determine a full length gene sequence.

Conveniently, such sequencing is performed, for example, using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL*, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989). (see  
15 in particular Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70). Direct genomic DNA sequencing may also be performed to obtain a full length gene sequence. Illustrative of the invention, each polynucleotide set out in SEQ ID NO:5 was discovered in a DNA library derived from *Neisseria meningitidis*.

20 Moreover, the DNA sequence set out in SEQ ID NO:5 contains an open reading frame encoding a protein having about the number of amino acid residues set forth in SEQ ID NO:6 with a deduced molecular weight that can be calculated using amino acid residue molecular weight values well known to those skilled in the art.

25 The polynucleotide of SEQ ID NO:5, between the start codon at nucleotide number 1 and the stop codon which begins at nucleotide number 418 of SEQ ID NO:5, encodes the polypeptide of SEQ ID NO:6.

In a further aspect, the present invention provides for an isolated polynucleotide comprising  
30 or consisting of:

- (a) a polynucleotide sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO:5 over the entire length of SEQ ID NO:5; or
- (b) a polynucleotide sequence encoding a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or 100% exact, to the amino acid sequence of SEQ ID NO:6 over the entire length of SEQ ID NO:6.

A polynucleotide encoding a polypeptide of the present invention, including homologs and orthologs from species other than *Neisseria meningitidis*, may be obtained by a process which comprises the steps of screening an appropriate library under stringent hybridization conditions (for example, using a temperature in the range of 45 – 65°C and an SDS concentration from 0.1 – 1%) with a labeled or detectable probe consisting of or comprising the sequence of SEQ ID NO:5 or a fragment thereof; and isolating a full-length gene and/or genomic clones containing said polynucleotide sequence.

The invention provides a polynucleotide sequence identical over its entire length to a coding sequence (open reading frame) in SEQ ID NO:5. Also provided by the invention is a coding sequence for a mature polypeptide or a fragment thereof, by itself as well as a coding sequence for a mature polypeptide or a fragment in reading frame with another coding sequence, such as a sequence encoding a leader or secretory sequence, a pre-, or pro- or prepro-protein sequence. The polynucleotide of the invention may also contain at least one non-coding sequence, including for example, but not limited to at least one non-coding 5' and 3' sequence, such as the transcribed but non-translated sequences, termination signals (such as rho-dependent and rho-independent termination signals), ribosome binding sites, Kozak sequences, sequences that stabilize mRNA, introns, and polyadenylation signals. The polynucleotide sequence may also comprise additional coding sequence encoding additional amino acids. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain embodiments of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz



5 *et al.*, *Proc. Natl. Acad. Sci., USA* 86: 821-824 (1989), or an HA peptide tag (Wilson *et al.*, *Cell* 37: 767 (1984), both of which may be useful in purifying polypeptide sequence fused to them. Polynucleotides of the invention also include, but are not limited to, polynucleotides comprising a structural gene and its naturally associated sequences that control gene expression.

The nucleotide sequence encoding BASB060 polypeptide of SEQ ID NO:6 may be identical to the polypeptide encoding sequence contained in nucleotides 1 to 417 of SEQ ID NO:5. Alternatively it may be a sequence, which as a result of the redundancy (degeneracy) of the genetic code, also encodes the polypeptide of SEQ ID NO:6.

10 The term "polynucleotide encoding a polypeptide" as used herein encompasses polynucleotides that include a sequence encoding a polypeptide of the invention, particularly a bacterial polypeptide and more particularly a polypeptide of the *Neisseria meningitidis* BASB060 having an amino acid sequence set out in SEQ ID NO:6. The term also  
15 encompasses polynucleotides that include a single continuous region or discontinuous regions encoding the polypeptide (for example, polynucleotides interrupted by integrated phage, an integrated insertion sequence, an integrated vector sequence, an integrated transposon sequence, or due to RNA editing or genomic DNA reorganization) together with additional regions, that also may contain coding and/or non-coding sequences.

20 The invention further relates to variants of the polynucleotides described herein that encode variants of a polypeptide having a deduced amino acid sequence of SEQ ID NO:6. Fragments of polynucleotides of the invention may be used, for example, to synthesize full-length polynucleotides of the invention.

25 Further particularly preferred embodiments are polynucleotides encoding BASB060 variants, that have the amino acid sequence of BASB060 polypeptide of SEQ ID NO:6 in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, modified, deleted and/or added, in any combination. Especially preferred among these are silent

substitutions, additions and deletions that do not alter the properties and activities of BASB060 polypeptide.

Further preferred embodiments of the invention are polynucleotides that are at least 85% identical over their entire length to a polynucleotide encoding BASB060 polypeptide having an amino acid sequence set out in SEQ ID NO:6 and polynucleotides that are complementary to such polynucleotides. In this regard, polynucleotides at least 90% identical over their entire length to the same are particularly preferred, and among these particularly preferred polynucleotides, those with at least 95% are especially preferred. Furthermore, those with at least 97% are highly preferred among those with at least 95%, and among these those with at least 98% and at least 99% are particularly highly preferred, with at least 99% being the more preferred.

Preferred embodiments are polynucleotides encoding polypeptides that retain substantially the same biological function or activity as the mature polypeptide encoded by a DNA of SEQ ID NO:5.

In accordance with certain preferred embodiments of this invention there are provided polynucleotides that hybridize, particularly under stringent conditions, to BASB060 polynucleotide sequences, such as those polynucleotides in SEQ ID NO:5.

The invention further relates to polynucleotides that hybridize to the polynucleotide sequences provided herein. In this regard, the invention especially relates to polynucleotides that hybridize under stringent conditions to the polynucleotides described herein. As herein used, the terms "stringent conditions" and "stringent hybridization conditions" mean hybridization occurring only if there is at least 95% and preferably at least 97% identity between the sequences. A specific example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml of denatured, sheared salmon sperm DNA,

followed by washing the hybridization support in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein. Solution hybridization may also be used with the

5 polynucleotide sequences provided by the invention.

The invention also provides a polynucleotide consisting of or comprising a polynucleotide sequence obtained by screening an appropriate library containing the complete gene for a polynucleotide sequence set forth in SEQ ID NO:5 under stringent hybridization conditions

10 with a probe having the sequence of said polynucleotide sequence set forth in SEQ ID NO:5 or a fragment thereof; and isolating said polynucleotide sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers fully described elsewhere herein.

15 As discussed elsewhere herein regarding polynucleotide assays of the invention, for instance, the polynucleotides of the invention, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding BASB060 and to isolate cDNA and genomic clones of other genes that have a high identity, particularly high sequence identity, to the BASB060 gene. Such probes generally will comprise at least 15

20 nucleotide residues or base pairs. Preferably, such probes will have at least 30 nucleotide residues or base pairs and may have at least 50 nucleotide residues or base pairs. Particularly preferred probes will have at least 20 nucleotide residues or base pairs and will have less than 30 nucleotide residues or base pairs.

25 A coding region of a BASB060 gene may be isolated by screening using a DNA sequence provided in SEQ ID NO:5 to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine which members of the library the probe hybridizes to.

It is an object of the invention to provide polynucleotides that encode BASB061 polypeptides, particularly polynucleotides that encode the polypeptide herein designated BASB061.

- 5 In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding BASB061 polypeptides comprising a sequence set out in SEQ ID NO:7 which includes a full length gene, or a variant thereof.

10 The BASB061 polynucleotide provided in SEQ ID NO:7 is the BASB061 polynucleotide from *Neisseria meningitidis* strains ATCC13090.

As a further aspect of the invention there are provided isolated nucleic acid molecules encoding and/or expressing BASB061 polypeptides and polynucleotides, particularly *Neisseria meningitidis* BASB061 polypeptides and polynucleotides, including, for  
15 example, unprocessed RNAs, ribozyme RNAs, mRNAs, cDNAs, genomic DNAs, B- and Z-DNAs. Further embodiments of the invention include biologically, diagnostically, prophylactically, clinically or therapeutically useful polynucleotides and polypeptides, and variants thereof, and compositions comprising the same.

- 20 Another aspect of the invention relates to isolated polynucleotides, including at least one full length gene, that encodes a BASB061 polypeptide having a deduced amino acid sequence of SEQ ID NO:8 and polynucleotides closely related thereto and variants thereof.

25 In another particularly preferred embodiment of the invention there is a BASB061 polypeptide from *Neisseria meningitidis* comprising or consisting of an amino acid sequence of SEQ ID NO:8 or a variant thereof.

30 Using the information provided herein, such as a polynucleotide sequence set out in SEQ ID NO:7 a polynucleotide of the invention encoding BASB061 polypeptide may be obtained using standard cloning and screening methods, such as those for cloning and sequencing



- (a) a polynucleotide sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO:7 over the entire length of SEQ ID NO:7; or
- (b) a polynucleotide sequence encoding a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or 100% exact, to the amino acid sequence of SEQ ID NO:8 over the entire length of SEQ ID NO:8.

A polynucleotide encoding a polypeptide of the present invention, including homologs and orthologs from species other than *Neisseria meningitidis*, may be obtained by a process which comprises the steps of screening an appropriate library under stringent hybridization conditions (for example, using a temperature in the range of 45 – 65°C and an SDS concentration from 0.1 – 1%) with a labeled or detectable probe consisting of or comprising the sequence of SEQ ID NO:7 or a fragment thereof; and isolating a full-length gene and/or genomic clones containing said polynucleotide sequence.

The invention provides a polynucleotide sequence identical over its entire length to a coding sequence (open reading frame) in SEQ ID NO:7. Also provided by the invention is a coding sequence for a mature polypeptide or a fragment thereof, by itself as well as a coding sequence for a mature polypeptide or a fragment in reading frame with another coding sequence, such as a sequence encoding a leader or secretory sequence, a pre-, or pro- or prepro-protein sequence. The polynucleotide of the invention may also contain at least one non-coding sequence, including for example, but not limited to at least one non-coding 5' and 3' sequence, such as the transcribed but non-translated sequences, termination signals (such as rho-dependent and rho-independent termination signals), ribosome binding sites, Kozak sequences, sequences that stabilize mRNA, introns, and polyadenylation signals. The polynucleotide sequence may also comprise additional coding sequence encoding additional amino acids. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain embodiments of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz

*et al.*, *Proc. Natl. Acad. Sci., USA* 86: 821-824 (1989), or an HA peptide tag (Wilson *et al.*, *Cell* 37: 767 (1984), both of which may be useful in purifying polypeptide sequence fused to them. Polynucleotides of the invention also include, but are not limited to, polynucleotides comprising a structural gene and its naturally associated sequences that control gene expression.

The nucleotide sequence encoding BASB061 polypeptide of SEQ ID NO:8 may be identical to the polypeptide encoding sequence contained in nucleotides 1 to 513 of SEQ ID NO:7. Alternatively it may be a sequence, which as a result of the redundancy (degeneracy) of the genetic code, also encodes the polypeptide of SEQ ID NO:8.

The term "polynucleotide encoding a polypeptide" as used herein encompasses polynucleotides that include a sequence encoding a polypeptide of the invention, particularly a bacterial polypeptide and more particularly a polypeptide of the *Neisseria meningitidis* BASB061 having an amino acid sequence set out in SEQ ID NO:8. The term also encompasses polynucleotides that include a single continuous region or discontinuous regions encoding the polypeptide (for example, polynucleotides interrupted by integrated phage, an integrated insertion sequence, an integrated vector sequence, an integrated transposon sequence, or due to RNA editing or genomic DNA reorganization) together with additional regions, that also may contain coding and/or non-coding sequences.

The invention further relates to variants of the polynucleotides described herein that encode variants of a polypeptide having a deduced amino acid sequence of SEQ ID NO:8.

Fragments of polynucleotides of the invention may be used, for example, to synthesize full-length polynucleotides of the invention.

Further particularly preferred embodiments are polynucleotides encoding BASB061 variants, that have the amino acid sequence of BASB061 polypeptide of SEQ ID NO:8 in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, modified, deleted and/or added, in any combination. Especially preferred among these are silent

substitutions, additions and deletions that do not alter the properties and activities of BASB061 polypeptide.

Further preferred embodiments of the invention are polynucleotides that are at least 85% identical over their entire length to a polynucleotide encoding BASB061 polypeptide having an amino acid sequence set out in SEQ ID NO:8 and polynucleotides that are complementary to such polynucleotides. In this regard, polynucleotides at least 90% identical over their entire length to the same are particularly preferred, and among these particularly preferred polynucleotides, those with at least 95% are especially preferred. Furthermore, those with at least 97% are highly preferred among those with at least 95%, and among these those with at least 98% and at least 99% are particularly highly preferred, with at least 99% being the more preferred.

Preferred embodiments are polynucleotides encoding polypeptides that retain substantially the same biological function or activity as the mature polypeptide encoded by a DNA of SEQ ID NO:7.

In accordance with certain preferred embodiments of this invention there are provided polynucleotides that hybridize, particularly under stringent conditions, to BASB061 polynucleotide sequences, such as those polynucleotides in SEQ ID NO:7.

The invention further relates to polynucleotides that hybridize to the polynucleotide sequences provided herein. In this regard, the invention especially relates to polynucleotides that hybridize under stringent conditions to the polynucleotides described herein. As herein used, the terms "stringent conditions" and "stringent hybridization conditions" mean hybridization occurring only if there is at least 95% and preferably at least 97% identity between the sequences. A specific example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml of denatured, sheared salmon sperm DNA,



followed by washing the hybridization support in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein. Solution hybridization may also be used with the  
5 polynucleotide sequences provided by the invention.

The invention also provides a polynucleotide consisting of or comprising a polynucleotide sequence obtained by screening an appropriate library containing the complete gene for a polynucleotide sequence set forth in SEQ ID NO:7 under stringent hybridization conditions  
10 with a probe having the sequence of said polynucleotide sequence set forth in SEQ ID NO:7 or a fragment thereof; and isolating said polynucleotide sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers fully described elsewhere herein.

As discussed elsewhere herein regarding polynucleotide assays of the invention, for instance, the polynucleotides of the invention, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding BASB061 and to isolate cDNA and genomic clones of other genes that have a high identity, particularly high sequence identity, to the BASB061 gene. Such probes generally will comprise at least 15  
15 nucleotide residues or base pairs. Preferably, such probes will have at least 30 nucleotide residues or base pairs and may have at least 50 nucleotide residues or base pairs. Particularly preferred probes will have at least 20 nucleotide residues or base pairs and will have less than 30 nucleotide residues or base pairs.

A coding region of a BASB061 gene may be isolated by screening using a DNA sequence provided in SEQ ID NO:7 to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine which members of the library the probe hybridizes to.  
25

It is an object of the invention to provide polynucleotides that encode BASB063 polypeptides, particularly polynucleotides that encode the polypeptide herein designated BASB063.

- 5 In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding BASB063 polypeptides comprising a sequence set out in SEQ ID NO:9 which includes a full length gene, or a variant thereof.

- 10 The BASB063 polynucleotide provided in SEQ ID NO:9 is the BASB063 polynucleotide from *Neisseria meningitidis* strains ATCC13090.

- As a further aspect of the invention there are provided isolated nucleic acid molecules encoding and/or expressing BASB063 polypeptides and polynucleotides, particularly *Neisseria meningitidis* BASB063 polypeptides and polynucleotides, including, for  
15 example, unprocessed RNAs, ribozyme RNAs, mRNAs, cDNAs, genomic DNAs, B- and Z-DNAs. Further embodiments of the invention include biologically, diagnostically, prophylactically, clinically or therapeutically useful polynucleotides and polypeptides, and variants thereof, and compositions comprising the same.
- 20 Another aspect of the invention relates to isolated polynucleotides, including at least one full length gene, that encodes a BASB063 polypeptide having a deduced amino acid sequence of SEQ ID NO:10 and polynucleotides closely related thereto and variants thereof.

- 25 In another particularly preferred embodiment of the invention there is a BASB063 polypeptide from *Neisseria meningitidis* comprising or consisting of an amino acid sequence of SEQ ID NO:10 or a variant thereof.

- Using the information provided herein, such as a polynucleotide sequence set out in SEQ ID NO:9 a polynucleotide of the invention encoding BASB063 polypeptide may be obtained  
30 using standard cloning and screening methods, such as those for cloning and sequencing

chromosomal DNA fragments from bacteria using *Neisseria meningitidis* cells as starting material, followed by obtaining a full length clone. For example, to obtain a polynucleotide sequence of the invention, such as a polynucleotide sequence given in SEQ ID NO:9 typically a library of clones of chromosomal DNA of *Neisseria meningitidis* in *E.coli* or  
5 some other suitable host is probed with a radiolabeled oligonucleotide, preferably a 17-mer or longer, derived from a partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using stringent hybridization conditions. By sequencing the individual clones thus identified by hybridization with sequencing primers designed from the original polypeptide or polynucleotide sequence it is then possible to extend the  
10 polynucleotide sequence in both directions to determine a full length gene sequence. Conveniently, such sequencing is performed, for example, using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL*, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989). (see  
15 in particular Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70). Direct genomic DNA sequencing may also be performed to obtain a full length gene sequence. Illustrative of the invention, each polynucleotide set out in SEQ ID NO:9 was discovered in a DNA library derived from *Neisseria meningitidis*.

20 Moreover, the DNA sequence set out in SEQ ID NO:9 contains an open reading frame encoding a protein having about the number of amino acid residues set forth in SEQ ID NO:10 with a deduced molecular weight that can be calculated using amino acid residue molecular weight values well known to those skilled in the art.

25 The polynucleotide of SEQ ID NO:9, between the start codon at nucleotide number 1 and the stop codon which begins at nucleotide number 814 of SEQ ID NO:9, encodes the polypeptide of SEQ ID NO:10.

In a further aspect, the present invention provides for an isolated polynucleotide comprising  
30 or consisting of:

- (a) a polynucleotide sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO:9 over the entire length of SEQ ID NO:9; or
- (b) a polynucleotide sequence encoding a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or 100% exact, to the amino acid sequence of SEQ ID NO:10 over the entire length of SEQ ID NO:10.

A polynucleotide encoding a polypeptide of the present invention, including homologs and orthologs from species other than *Neisseria meningitidis*, may be obtained by a process which comprises the steps of screening an appropriate library under stringent hybridization conditions (for example, using a temperature in the range of 45 – 65°C and an SDS concentration from 0.1 – 1%) with a labeled or detectable probe consisting of or comprising the sequence of SEQ ID NO:9 or a fragment thereof; and isolating a full-length gene and/or genomic clones containing said polynucleotide sequence.

The invention provides a polynucleotide sequence identical over its entire length to a coding sequence (open reading frame) in SEQ ID NO:9. Also provided by the invention is a coding sequence for a mature polypeptide or a fragment thereof, by itself as well as a coding sequence for a mature polypeptide or a fragment in reading frame with another coding sequence, such as a sequence encoding a leader or secretory sequence, a pre-, or pro- or prepro-protein sequence. The polynucleotide of the invention may also contain at least one non-coding sequence, including for example, but not limited to at least one non-coding 5' and 3' sequence, such as the transcribed but non-translated sequences, termination signals (such as rho-dependent and rho-independent termination signals), ribosome binding sites, Kozak sequences, sequences that stabilize mRNA, introns, and polyadenylation signals. The polynucleotide sequence may also comprise additional coding sequence encoding additional amino acids. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain embodiments of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz

*et al.*, *Proc. Natl. Acad. Sci., USA* 86: 821-824 (1989), or an HA peptide tag (Wilson *et al.*, *Cell* 37: 767 (1984), both of which may be useful in purifying polypeptide sequence fused to them. Polynucleotides of the invention also include, but are not limited to, polynucleotides comprising a structural gene and its naturally associated sequences that control gene expression.

The nucleotide sequence encoding BASB063 polypeptide of SEQ ID NO:10 may be identical to the polypeptide encoding sequence contained in nucleotides 1 to 813 of SEQ ID NO:9. Alternatively it may be a sequence, which as a result of the redundancy (degeneracy) of the genetic code, also encodes the polypeptide of SEQ ID NO:10.

The term "polynucleotide encoding a polypeptide" as used herein encompasses polynucleotides that include a sequence encoding a polypeptide of the invention, particularly a bacterial polypeptide and more particularly a polypeptide of the *Neisseria meningitidis* BASB063 having an amino acid sequence set out in SEQ ID NO:10. The term also encompasses polynucleotides that include a single continuous region or discontinuous regions encoding the polypeptide (for example, polynucleotides interrupted by integrated phage, an integrated insertion sequence, an integrated vector sequence, an integrated transposon sequence, or due to RNA editing or genomic DNA reorganization) together with additional regions, that also may contain coding and/or non-coding sequences.

The invention further relates to variants of the polynucleotides described herein that encode variants of a polypeptide having a deduced amino acid sequence of SEQ ID NO:10.

Fragments of polynucleotides of the invention may be used, for example, to synthesize full-length polynucleotides of the invention.

Further particularly preferred embodiments are polynucleotides encoding BASB063 variants, that have the amino acid sequence of BASB063 polypeptide of SEQ ID NO:10 in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, modified, deleted and/or added, in any combination. Especially preferred among these are silent

substitutions, additions and deletions that do not alter the properties and activities of BASB063 polypeptide.

Further preferred embodiments of the invention are polynucleotides that are at least 85% identical over their entire length to a polynucleotide encoding BASB063 polypeptide having an amino acid sequence set out in SEQ ID NO:10 and polynucleotides that are complementary to such polynucleotides. In this regard, polynucleotides at least 90% identical over their entire length to the same are particularly preferred, and among these particularly preferred polynucleotides, those with at least 95% are especially preferred. Furthermore, those with at least 97% are highly preferred among those with at least 95%, and among these those with at least 98% and at least 99% are particularly highly preferred, with at least 99% being the more preferred.

Preferred embodiments are polynucleotides encoding polypeptides that retain substantially  
15 the same biological function or activity as the mature polypeptide encoded by a DNA of SEQ  
ID NO:9.

In accordance with certain preferred embodiments of this invention there are provided polynucleotides that hybridize, particularly under stringent conditions, to BASB063  
20 polynucleotide sequences, such as those polynucleotides in SEQ ID NO:9.

The invention further relates to polynucleotides that hybridize to the polynucleotide sequences provided herein. In this regard, the invention especially relates to polynucleotides that hybridize under stringent conditions to the polynucleotides described herein. As herein  
25 used, the terms "stringent conditions" and "stringent hybridization conditions" mean hybridization occurring only if there is at least 95% and preferably at least 97% identity between the sequences. A specific example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution,  
30 10% dextran sulfate, and 20 micrograms/ml of denatured, sheared salmon sperm DNA,

followed by washing the hybridization support in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein. Solution hybridization may also be used with the  
5 polynucleotide sequences provided by the invention.

The invention also provides a polynucleotide consisting of or comprising a polynucleotide sequence obtained by screening an appropriate library containing the complete gene for a polynucleotide sequence set forth in SEQ ID NO:9 under stringent hybridization conditions  
10 with a probe having the sequence of said polynucleotide sequence set forth in SEQ ID NO:9 or a fragment thereof; and isolating said polynucleotide sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers fully described elsewhere herein.

As discussed elsewhere herein regarding polynucleotide assays of the invention, for instance, the polynucleotides of the invention, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding BASB063 and to isolate cDNA and genomic clones of other genes that have a high identity, particularly high sequence identity, to the BASB063 gene. Such probes generally will comprise at least 15  
15 nucleotide residues or base pairs. Preferably, such probes will have at least 30 nucleotide residues or base pairs and may have at least 50 nucleotide residues or base pairs. Particularly preferred probes will have at least 20 nucleotide residues or base pairs and will have less than 30 nucleotide residues or base pairs.

A coding region of a BASB063 gene may be isolated by screening using a DNA sequence provided in SEQ ID NO:9 to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine which members of the library the probe hybridizes to.  
25

It is an object of the invention to provide polynucleotides that encode BASB065 polypeptides, particularly polynucleotides that encode the polypeptide herein designated BASB065.

- 5 In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding BASB065 polypeptides comprising a sequence set out in SEQ ID NO:11 which includes a full length gene, or a variant thereof.

- 10 The BASB065 polynucleotide provided in SEQ ID NO:11 is the BASB065 polynucleotide from *Neisseria meningitidis* strains ATCC13090.

- 15 As a further aspect of the invention there are provided isolated nucleic acid molecules encoding and/or expressing BASB065 polypeptides and polynucleotides, particularly *Neisseria meningitidis* BASB065 polypeptides and polynucleotides, including, for example, unprocessed RNAs, ribozyme RNAs, mRNAs, cDNAs, genomic DNAs, B- and Z-DNAs. Further embodiments of the invention include biologically, diagnostically, prophylactically, clinically or therapeutically useful polynucleotides and polypeptides, and variants thereof, and compositions comprising the same.
- 20 Another aspect of the invention relates to isolated polynucleotides, including at least one full length gene, that encodes a BASB065 polypeptide having a deduced amino acid sequence of SEQ ID NO:12 and polynucleotides closely related thereto and variants thereof.

- 25 In another particularly preferred embodiment of the invention there is a BASB065 polypeptide from *Neisseria meningitidis* comprising or consisting of an amino acid sequence of SEQ ID NO:12 or a variant thereof.

- 30 Using the information provided herein, such as a polynucleotide sequence set out in SEQ ID NO:11 a polynucleotide of the invention encoding BASB065 polypeptide may be obtained using standard cloning and screening methods, such as those for cloning and sequencing



- chromosomal DNA fragments from bacteria using *Neisseria meningitidis* cells as starting material, followed by obtaining a full length clone. For example, to obtain a polynucleotide sequence of the invention, such as a polynucleotide sequence given in SEQ ID NO:11 typically a library of clones of chromosomal DNA of *Neisseria meningitidis* in *E.coli* or
- 5 some other suitable host is probed with a radiolabeled oligonucleotide, preferably a 17-mer or longer, derived from a partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using stringent hybridization conditions. By sequencing the individual clones thus identified by hybridization with sequencing primers designed from the original polypeptide or polynucleotide sequence it is then possible to extend the
- 10 polynucleotide sequence in both directions to determine a full length gene sequence. Conveniently, such sequencing is performed, for example, using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL*, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989). (see
- 15 in particular Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70). Direct genomic DNA sequencing may also be performed to obtain a full length gene sequence. Illustrative of the invention, each polynucleotide set out in SEQ ID NO:11 was discovered in a DNA library derived from *Neisseria meningitidis*.
- 20 Moreover, the DNA sequence set out in SEQ ID NO:11 contains an open reading frame encoding a protein having about the number of amino acid residues set forth in SEQ ID NO:12 with a deduced molecular weight that can be calculated using amino acid residue molecular weight values well known to those skilled in the art.
- 25 The polynucleotide of SEQ ID NO:11, between the start codon at nucleotide number 1 and the stop codon which begins at nucleotide number 715 of SEQ ID NO:11, encodes the polypeptide of SEQ ID NO:12.

- In a further aspect, the present invention provides for an isolated polynucleotide comprising
- 30 or consisting of:

- (a) a polynucleotide sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO:11 over the entire length of SEQ ID NO:11; or
- (b) a polynucleotide sequence encoding a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or 100% exact, to the amino acid sequence of SEQ ID NO:12 over the entire length of SEQ ID NO:12.

A polynucleotide encoding a polypeptide of the present invention, including homologs and orthologs from species other than *Neisseria meningitidis*, may be obtained by a process which comprises the steps of screening an appropriate library under stringent hybridization conditions (for example, using a temperature in the range of 45 – 65°C and an SDS concentration from 0.1 – 1%) with a labeled or detectable probe consisting of or comprising the sequence of SEQ ID NO:11 or a fragment thereof; and isolating a full-length gene and/or genomic clones containing said polynucleotide sequence.

The invention provides a polynucleotide sequence identical over its entire length to a coding sequence (open reading frame) in SEQ ID NO:11. Also provided by the invention is a coding sequence for a mature polypeptide or a fragment thereof, by itself as well as a coding sequence for a mature polypeptide or a fragment in reading frame with another coding sequence, such as a sequence encoding a leader or secretory sequence, a pre-, or pro- or prepro-protein sequence. The polynucleotide of the invention may also contain at least one non-coding sequence, including for example, but not limited to at least one non-coding 5' and 3' sequence, such as the transcribed but non-translated sequences, termination signals (such as rho-dependent and rho-independent termination signals), ribosome binding sites, Kozak sequences, sequences that stabilize mRNA, introns, and polyadenylation signals. The polynucleotide sequence may also comprise additional coding sequence encoding additional amino acids. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain embodiments of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz



substitutions, additions and deletions, that do not alter the properties and activities of BASB065 polypeptide.

Further preferred embodiments of the invention are polynucleotides that are at least 85% identical over their entire length to a polynucleotide encoding BASB065 polypeptide having an amino acid sequence set out in SEQ ID NO:12 and polynucleotides that are complementary to such polynucleotides. In this regard, polynucleotides at least 90% identical over their entire length to the same are particularly preferred, and among these particularly preferred polynucleotides, those with at least 95% are especially preferred. Furthermore, those with at least 97% are highly preferred among those with at least 95%, and among these those with at least 98% and at least 99% are particularly highly preferred, with at least 99% being the more preferred.

Preferred embodiments are polynucleotides encoding polypeptides that retain substantially the same biological function or activity as the mature polypeptide encoded by a DNA of SEQ ID NO:11.

In accordance with certain preferred embodiments of this invention there are provided polynucleotides that hybridize, particularly under stringent conditions, to BASB065 polynucleotide sequences, such as those polynucleotides in SEQ ID NO:11.

The invention further relates to polynucleotides that hybridize to the polynucleotide sequences provided herein. In this regard, the invention especially relates to polynucleotides that hybridize under stringent conditions to the polynucleotides described herein. As herein used, the terms "stringent conditions" and "stringent hybridization conditions" mean hybridization occurring only if there is at least 95% and preferably at least 97% identity between the sequences. A specific example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml of denatured, sheared salmon sperm DNA,

followed by washing the hybridization support in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein. Solution hybridization may also be used with the

5 polynucleotide sequences provided by the invention.

The invention also provides a polynucleotide consisting of or comprising a polynucleotide sequence obtained by screening an appropriate library containing the complete gene for a polynucleotide sequence set forth in SEQ ID NO:11 under stringent hybridization

10 conditions with a probe having the sequence of said polynucleotide sequence set forth in SEQ ID NO:11 or a fragment thereof; and isolating said polynucleotide sequence.

Fragments useful for obtaining such a polynucleotide include, for example, probes and primers fully described elsewhere herein.

15 As discussed elsewhere herein regarding polynucleotide assays of the invention, for instance, the polynucleotides of the invention, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding BASB065 and to isolate cDNA and genomic clones of other genes that have a high identity, particularly high sequence identity, to the BASB065 gene. Such probes generally will comprise at least 15

20 nucleotide residues or base pairs. Preferably, such probes will have at least 30 nucleotide residues or base pairs and may have at least 50 nucleotide residues or base pairs. Particularly preferred probes will have at least 20 nucleotide residues or base pairs and will have less than 30 nucleotide residues or base pairs.

25 A coding region of a BASB065 gene may be isolated by screening using a DNA sequence provided in SEQ ID NO:11 to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine which members of the library the probe hybridizes to.

It is an object of the invention to provide polynucleotides that encode BASB066 polypeptides, particularly polynucleotides that encode the polypeptide herein designated BASB066.

- 5 In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding BASB066 polypeptides comprising a sequence set out in SEQ ID NO:13 which includes a full length gene, or a variant thereof.

- 10 The BASB066 polynucleotide provided in SEQ ID NO:13 is the BASB066 polynucleotide from *Neisseria meningitidis* strains ATCC13090.

- 15 As a further aspect of the invention there are provided isolated nucleic acid molecules encoding and/or expressing BASB066 polypeptides and polynucleotides, particularly *Neisseria meningitidis* BASB066 polypeptides and polynucleotides, including, for example, unprocessed RNAs, ribozyme RNAs, mRNAs, cDNAs, genomic DNAs, B- and Z-DNAs. Further embodiments of the invention include biologically, diagnostically, prophylactically, clinically or therapeutically useful polynucleotides and polypeptides, and variants thereof, and compositions comprising the same.

- 20 Another aspect of the invention relates to isolated polynucleotides, including at least one full length gene, that encodes a BASB066 polypeptide having a deduced amino acid sequence of SEQ ID NO:14 and polynucleotides closely related thereto and variants thereof.

- 25 In another particularly preferred embodiment of the invention there is a BASB066 polypeptide from *Neisseria meningitidis* comprising or consisting of an amino acid sequence of SEQ ID NO:14 or a variant thereof.

- 30 Using the information provided herein, such as a polynucleotide sequence set out in SEQ ID NO:13 a polynucleotide of the invention encoding BASB066 polypeptide may be obtained using standard cloning and screening methods, such as those for cloning and sequencing

chromosomal DNA fragments from bacteria using *Neisseria meningitidis* cells as starting material, followed by obtaining a full length clone. For example, to obtain a polynucleotide sequence of the invention, such as a polynucleotide sequence given in SEQ ID NO:13

typically a library of clones of chromosomal DNA of *Neisseria meningitidis* in *E.coli* or  
5 some other suitable host is probed with a radiolabeled oligonucleotide, preferably a 17-mer or longer, derived from a partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using stringent hybridization conditions. By sequencing the individual clones thus identified by hybridization with sequencing primers designed from the original polypeptide or polynucleotide sequence it is then possible to extend the  
10 polynucleotide sequence in both directions to determine a full length gene sequence.

Conveniently, such sequencing is performed, for example, using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL*, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989). (see  
15 in particular Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70). Direct genomic DNA sequencing may also be performed to obtain a full length gene sequence. Illustrative of the invention, each polynucleotide set out in SEQ ID NO:13 was discovered in a DNA library derived from *Neisseria meningitidis*.

20 Moreover, the DNA sequence set out in SEQ ID NO:13 contains an open reading frame encoding a protein having about the number of amino acid residues set forth in SEQ ID NO:14 with a deduced molecular weight that can be calculated using amino acid residue molecular weight values well known to those skilled in the art.

25 The polynucleotide of SEQ ID NO:13, between the start codon at nucleotide number 1 and the stop codon which begins at nucleotide number 1174 of SEQ ID NO:13, encodes the polypeptide of SEQ ID NO:14.

In a further aspect, the present invention provides for an isolated polynucleotide comprising  
30 or consisting of:

- (a) a polynucleotide sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO:13 over the entire length of SEQ ID NO:13; or
- (b) a polynucleotide sequence encoding a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or 100% exact, to the amino acid sequence of SEQ ID NO:14 over the entire length of SEQ ID NO:14.

A polynucleotide encoding a polypeptide of the present invention, including homologs and orthologs from species other than *Neisseria meningitidis*, may be obtained by a process which comprises the steps of screening an appropriate library under stringent hybridization conditions (for example, using a temperature in the range of 45 – 65°C and an SDS concentration from 0.1 – 1%) with a labeled or detectable probe consisting of or comprising the sequence of SEQ ID NO:13 or a fragment thereof; and isolating a full-length gene and/or genomic clones containing said polynucleotide sequence.

The invention provides a polynucleotide sequence identical over its entire length to a coding sequence (open reading frame) in SEQ ID NO:13. Also provided by the invention is a coding sequence for a mature polypeptide or a fragment thereof, by itself as well as a coding sequence for a mature polypeptide or a fragment in reading frame with another coding sequence, such as a sequence encoding a leader or secretory sequence, a pre-, or pro- or prepro-protein sequence. The polynucleotide of the invention may also contain at least one non-coding sequence, including for example, but not limited to at least one non-coding 5' and 3' sequence, such as the transcribed but non-translated sequences, termination signals (such as rho-dependent and rho-independent termination signals), ribosome binding sites, Kozak sequences, sequences that stabilize mRNA, introns, and polyadenylation signals. The polynucleotide sequence may also comprise additional coding sequence encoding additional amino acids. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain embodiments of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz



5 *et al.*, *Proc. Natl. Acad. Sci., USA* 86: 821-824 (1989), or an HA peptide tag (Wilson *et al.*, *Cell* 37: 767 (1984), both of which may be useful in purifying polypeptide sequence fused to them. Polynucleotides of the invention also include, but are not limited to, polynucleotides comprising a structural gene and its naturally associated sequences that control gene expression.

10 The nucleotide sequence encoding BASB066 polypeptide of SEQ ID NO:14 may be identical to the polypeptide encoding sequence contained in nucleotides 1 to 1173 of SEQ ID NO:13. Alternatively it may be a sequence, which as a result of the redundancy (degeneracy) of the genetic code, also encodes the polypeptide of SEQ ID NO:14. The term "polynucleotide encoding a polypeptide" as used herein encompasses polynucleotides that include a sequence encoding a polypeptide of the invention, particularly a bacterial polypeptide and more particularly a polypeptide of the *Neisseria meningitidis* BASB066 having an amino acid sequence set out in SEQ ID NO:14. The term also  
15 encompasses polynucleotides that include a single continuous region or discontinuous regions encoding the polypeptide (for example, polynucleotides interrupted by integrated phage, an integrated insertion sequence, an integrated vector sequence, an integrated transposon sequence, or due to RNA editing or genomic DNA reorganization) together with additional regions, that also may contain coding and/or non-coding sequences.

20

The invention further relates to variants of the polynucleotides described herein that encode variants of a polypeptide having a deduced amino acid sequence of SEQ ID NO:14.

Fragments of polynucleotides of the invention may be used, for example, to synthesize full-length polynucleotides of the invention.

25

Further particularly preferred embodiments are polynucleotides encoding BASB066 variants, that have the amino acid sequence of BASB066 polypeptide of SEQ ID NO:14 in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, modified, deleted and/or added, in any combination. Especially preferred among these are silent

substitutions, additions and deletions, that do not alter the properties and activities of BASB066 polypeptide.

Further preferred embodiments of the invention are polynucleotides that are at least 85% identical over their entire length to a polynucleotide encoding BASB066 polypeptide having an amino acid sequence set out in SEQ ID NO:14 and polynucleotides that are complementary to such polynucleotides. In this regard, polynucleotides at least 90% identical over their entire length to the same are particularly preferred, and among these particularly preferred polynucleotides, those with at least 95% are especially preferred. Furthermore, those with at least 97% are highly preferred among those with at least 95%, and among these those with at least 98% and at least 99% are particularly highly preferred, with at least 99% being the more preferred.

Preferred embodiments are polynucleotides encoding polypeptides that retain substantially  
15 the same biological function or activity as the mature polypeptide encoded by a DNA of SEQ  
ID NO:13.

In accordance with certain preferred embodiments of this invention there are provided polynucleotides that hybridize, particularly under stringent conditions, to BASB066  
20 polynucleotide sequences, such as those polynucleotides in SEQ ID NO:13.

The invention further relates to polynucleotides that hybridize to the polynucleotide sequences provided herein. In this regard, the invention especially relates to polynucleotides that hybridize under stringent conditions to the polynucleotides described herein. As herein  
25 used, the terms "stringent conditions" and "stringent hybridization conditions" mean hybridization occurring only if there is at least 95% and preferably at least 97% identity between the sequences. A specific example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution,  
30 10% dextran sulfate, and 20 micrograms/ml of denatured, sheared salmon sperm DNA,



It is an object of the invention to provide polynucleotides that encode BASB071 polypeptides, particularly polynucleotides that encode the polypeptide herein designated BASB071.

- 5 In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding BASB071 polypeptides comprising a sequence set out in SEQ ID NO:15 which includes a full length gene, or a variant thereof.

The BASB071 polynucleotide provided in SEQ ID NO:15 is the BASB071  
10 polynucleotide from *Neisseria meningitidis* strains ATCC13090.

As a further aspect of the invention there are provided isolated nucleic acid molecules encoding and/or expressing BASB071 polypeptides and polynucleotides, particularly *Neisseria meningitidis* BASB071 polypeptides and polynucleotides, including, for  
15 example, unprocessed RNAs, ribozyme RNAs, mRNAs, cDNAs, genomic DNAs, B- and Z-DNAs. Further embodiments of the invention include biologically, diagnostically, prophylactically, clinically or therapeutically useful polynucleotides and polypeptides, and variants thereof, and compositions comprising the same.

- 20 Another aspect of the invention relates to isolated polynucleotides, including at least one full length gene, that encodes a BASB071 polypeptide having a deduced amino acid sequence of SEQ ID NO:16 and polynucleotides closely related thereto and variants thereof.

In another particularly preferred embodiment of the invention there is a BASB071  
25 polypeptide from *Neisseria meningitidis* comprising or consisting of an amino acid sequence of SEQ ID NO:16 or a variant thereof.

Using the information provided herein, such as a polynucleotide sequence set out in SEQ ID NO:15 a polynucleotide of the invention encoding BASB071 polypeptide may be obtained  
30 using standard cloning and screening methods, such as those for cloning and sequencing

chromosomal DNA fragments from bacteria using *Neisseria meningitidis* cells as starting material, followed by obtaining a full length clone. For example, to obtain a polynucleotide sequence of the invention, such as a polynucleotide sequence given in SEQ ID NO:15 typically a library of clones of chromosomal DNA of *Neisseria meningitidis* in *E.coli* or  
5 some other suitable host is probed with a radiolabeled oligonucleotide, preferably a 17-mer or longer, derived from a partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using stringent hybridization conditions. By sequencing the individual clones thus identified by hybridization with sequencing primers designed from the original polypeptide or polynucleotide sequence it is then possible to extend the  
10 polynucleotide sequence in both directions to determine a full length gene sequence. Conveniently, such sequencing is performed, for example, using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL*, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989). (see  
15 in particular Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70). Direct genomic DNA sequencing may also be performed to obtain a full length gene sequence. Illustrative of the invention, each polynucleotide set out in SEQ ID NO:15 was discovered in a DNA library derived from *Neisseria meningitidis*.

20 Moreover, the DNA sequence set out in SEQ ID NO:15 contains an open reading frame encoding a protein having about the number of amino acid residues set forth in SEQ ID NO:16 with a deduced molecular weight that can be calculated using amino acid residue molecular weight values well known to those skilled in the art.

25 The polynucleotide of SEQ ID NO:15, between the start codon at nucleotide number 1 and the stop codon which begins at nucleotide number 805 of SEQ ID NO:15, encodes the polypeptide of SEQ ID NO:16.

In a further aspect, the present invention provides for an isolated polynucleotide comprising  
30 or consisting of:

- (a) a polynucleotide sequence which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO:15 over the entire length of SEQ ID NO:15; or
- (b) a polynucleotide sequence encoding a polypeptide which has at least 85% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or 100% exact, to the amino acid sequence of SEQ ID NO:16 over the entire length of SEQ ID NO:16.

A polynucleotide encoding a polypeptide of the present invention, including homologs and orthologs from species other than *Neisseria meningitidis*, may be obtained by a process which comprises the steps of screening an appropriate library under stringent hybridization conditions (for example, using a temperature in the range of 45 – 65°C and an SDS concentration from 0.1 – 1%) with a labeled or detectable probe consisting of or comprising the sequence of SEQ ID NO:15 or a fragment thereof; and isolating a full-length gene and/or genomic clones containing said polynucleotide sequence.

The invention provides a polynucleotide sequence identical over its entire length to a coding sequence (open reading frame) in SEQ ID NO:15. Also provided by the invention is a coding sequence for a mature polypeptide or a fragment thereof, by itself as well as a coding sequence for a mature polypeptide or a fragment in reading frame with another coding sequence, such as a sequence encoding a leader or secretory sequence, a pre-, or pro- or prepro-protein sequence. The polynucleotide of the invention may also contain at least one non-coding sequence, including for example, but not limited to at least one non-coding 5' and 3' sequence, such as the transcribed but non-translated sequences, termination signals (such as rho-dependent and rho-independent termination signals), ribosome binding sites, Kozak sequences, sequences that stabilize mRNA, introns, and polyadenylation signals. The polynucleotide sequence may also comprise additional coding sequence encoding additional amino acids. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain embodiments of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz



substitutions, additions and deletions, that do not alter the properties and activities of BASB071 polypeptide.

Further preferred embodiments of the invention are polynucleotides that are at least 85% identical over their entire length to a polynucleotide encoding BASB071 polypeptide having an amino acid sequence set out in SEQ ID NO:16 and polynucleotides that are complementary to such polynucleotides. In this regard, polynucleotides at least 90% identical over their entire length to the same are particularly preferred, and among these particularly preferred polynucleotides, those with at least 95% are especially preferred. Furthermore, those with at least 97% are highly preferred among those with at least 95%, and among these those with at least 98% and at least 99% are particularly highly preferred, with at least 99% being the more preferred.

Preferred embodiments are polynucleotides encoding polypeptides that retain substantially the same biological function or activity as the mature polypeptide encoded by a DNA of SEQ ID NO:15.

In accordance with certain preferred embodiments of this invention there are provided polynucleotides that hybridize, particularly under stringent conditions, to BASB071 polynucleotide sequences, such as those polynucleotides in SEQ ID NO:15.

The invention further relates to polynucleotides that hybridize to the polynucleotide sequences provided herein. In this regard, the invention especially relates to polynucleotides that hybridize under stringent conditions to the polynucleotides described herein. As herein used, the terms "stringent conditions" and "stringent hybridization conditions" mean hybridization occurring only if there is at least 95% and preferably at least 97% identity between the sequences. A specific example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml of denatured, sheared salmon sperm DNA,





There are several methods available and well known to those skilled in the art to obtain full-length DNAs, or extend short DNAs, for example those based on the method of Rapid Amplification of cDNA ends (RACE) (see, for example, Frohman, *et al.*, *PNAS USA* 85: 8998-9002, 1988). Recent modifications of the technique, exemplified by the Marathon™ technology (Clontech Laboratories Inc.) for example, have significantly simplified the search for longer cDNAs. In the Marathon™ technology, cDNAs have been prepared from mRNA extracted from a chosen tissue and an 'adaptor' sequence ligated onto each end. Nucleic acid amplification (PCR) is then carried out to amplify the "missing" 5' end of the DNA using a combination of gene specific and adaptor specific oligonucleotide primers. The PCR reaction is then repeated using "nested" primers, that is, primers designed to anneal within the amplified product (typically an adaptor specific primer that anneals further 3' in the adaptor sequence and a gene specific primer that anneals further 5' in the selected gene sequence). The products of this reaction can then be analyzed by DNA sequencing and a full-length DNA constructed either by joining the product directly to the existing DNA to give a complete sequence, or carrying out a separate full-length PCR using the new sequence information for the design of the 5' primer.

The polynucleotides and polypeptides of the invention may be employed, for example, as  
20 research reagents and materials for discovery of treatments of and diagnostics for diseases,  
particularly human diseases, as further discussed herein relating to polynucleotide assays.

The polynucleotides of the invention that are oligonucleotides derived from a sequence of SEQ ID NOS:1 – 16 may be used in the processes herein as described, but preferably for PCR, to determine whether or not the polynucleotides identified herein in whole or in part are transcribed in bacteria in infected tissue. It is recognized that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained.

The invention also provides polynucleotides that encode a polypeptide that is the mature protein plus additional amino or carboxyl-terminal amino acids, or amino acids interior to the mature polypeptide (when the mature form has more than one polypeptide chain, for instance). Such sequences may play a role in processing of a protein from precursor to a mature form, may allow protein transport, may lengthen or shorten protein half-life or may facilitate manipulation of a protein for assay or production, among other things. As generally is the case *in vivo*, the additional amino acids may be processed away from the mature protein by cellular enzymes.

For each and every polynucleotide of the invention there is provided a polynucleotide complementary to it. It is preferred that these complementary polynucleotides are fully complementary to each polynucleotide with which they are complementary.

A precursor protein, having a mature form of the polypeptide fused to one or more prosequences may be an inactive form of the polypeptide. When prosequences are removed such inactive precursors generally are activated. Some or all of the prosequences may be removed before activation. Generally, such precursors are called proproteins.

In addition to the standard A, G, C, T/U representations for nucleotides, the term "N" may also be used in describing certain polynucleotides of the invention. "N" means that any of the four DNA or RNA nucleotides may appear at such a designated position in the DNA or RNA sequence, except it is preferred that N is not a nucleic acid that when taken in combination with adjacent nucleotide positions, when read in the correct reading frame, would have the effect of generating a premature termination codon in such reading frame.

In sum, a polynucleotide of the invention may encode a mature protein, a mature protein plus a leader sequence (which may be referred to as a preprotein), a precursor of a mature protein having one or more prosequences that are not the leader sequences of a preprotein, or a preproprotein, which is a precursor to a proprotein, having a leader sequence and one or more

prosequences, which generally are removed during processing steps that produce active and mature forms of the polypeptide.

In accordance with an aspect of the invention, there is provided the use of a polynucleotide  
5 of the invention for therapeutic or prophylactic purposes, in particular genetic  
immunization.

The use of a polynucleotide of the invention in genetic immunization will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscles (Wolff *et al.*, *Hum Mol Genet* (1992) 1: 363, Manthorpe *et al.*, *Hum. Gene Ther.* (1983) 4: 419), delivery of DNA complexed with specific protein carriers (Wu *et al.*, *J Biol Chem.* (1989) 264: 16985), coprecipitation of DNA with calcium phosphate (Benvenisty & Reshef, *PNAS USA*, (1986) 83: 9551), encapsulation of DNA in various forms of liposomes (Kaneda *et al.*, *Science* (1989) 243: 375), particle bombardment (Tang *et al.*, *Nature* (1992) 356:152, Eisenbraun *et al.*, *DNA Cell Biol* (1993) 12: 791) and *in vivo* infection using cloned retroviral vectors (Seeger *et al.*, *PNAS USA* (1984) 81: 5849).

## Vectors, Host Cells, Expression Systems

20

The invention also relates to vectors that comprise a polynucleotide or polynucleotides of the invention, host cells that are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the invention.

Recombinant polypeptides of the present invention may be prepared by processes well known in those skilled in the art from genetically engineered host cells comprising expression systems. Accordingly, in a further aspect, the present invention relates to expression systems that comprise a polynucleotide or polynucleotides of the present invention, to host cells which

are genetically engineered with such expression systems, and to the production of polypeptides of the invention by recombinant techniques.

For recombinant production of the polypeptides of the invention, host cells can be genetically engineered to incorporate expression systems or portions thereof or polynucleotides of the invention. Introduction of a polynucleotide into the host cell can be effected by methods described in many standard laboratory manuals, such as Davis, *et al.*, *BASIC METHODS IN MOLECULAR BIOLOGY*, (1986) and Sambrook, *et al.*, *MOLECULAR CLONING: A LABORATORY MANUAL*, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989), such as, calcium phosphate transfection, DEAE-dextran mediated transfection, transvection, microinjection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction and infection.

Representative examples of appropriate hosts include bacterial cells, such as cells of streptococci, staphylococci, enterococci, *E. coli*, streptomyces, cyanobacteria, *Bacillus subtilis*, *Moraxella catarrhalis*, *Haemophilus influenzae* and *Neisseria meningitidis*; fungal cells, such as cells of a yeast, *Kluveromyces*, *Saccharomyces*, a basidiomycete, *Candida albicans* and *Aspergillus*; insect cells such as cells of *Drosophila* S2 and *Spodoptera* Sf9; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, 293, CV-1 and Bowes melanoma cells; and plant cells, such as cells of a gymnosperm or angiosperm.

A great variety of expression systems can be used to produce the polypeptides of the invention. Such vectors include, among others, chromosomal-, episomal- and virus-derived vectors, for example, vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses, picornaviruses, retroviruses, and alphaviruses and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids. The expression system constructs may contain control regions that regulate as well as engender

expression. Generally, any system or vector suitable to maintain, propagate or express polynucleotides and/or to express a polypeptide in a host may be used for expression in this regard. The appropriate DNA sequence may be inserted into the expression system by any of a variety of well-known and routine techniques, such as, for example, those set forth in

5 Sambrook *et al.*, *MOLECULAR CLONING, A LABORATORY MANUAL*, (*supra*).

In recombinant expression systems in eukaryotes, for secretion of a translated protein into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment, appropriate secretion signals may be incorporated into the expressed polypeptide. These signals may be endogenous to the polypeptide or they may be heterologous signals.

Polypeptides of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid  
15 extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, ion metal affinity chromatography (IMAC) is employed for purification. Well known techniques for refolding proteins may be employed to regenerate active conformation when the  
20 polypeptide is denatured during intracellular synthesis, isolation and or purification.

The expression system may also be a recombinant live microorganism, such as a virus or bacterium. The gene of interest can be inserted into the genome of a live recombinant virus or bacterium. Inoculation and *in vivo* infection with this live vector will lead to *in vivo* expression of the antigen and induction of immune responses. Viruses and bacteria used for this purpose are for instance: poxviruses (e.g; vaccinia, fowlpox, canarypox), alphaviruses (Sindbis virus, Semliki Forest Virus, Venezuelan Equine Encephalitis Virus), adenoviruses, adeno-associated virus, picornaviruses (poliovirus, rhinovirus), herpesviruses (varicella zoster virus, etc), *Listeria*, *Salmonella*, *Shigella*, *Neisseria*, BCG.

These viruses and bacteria can be virulent, or attenuated in various ways in order to obtain live vaccines. Such live vaccines also form part of the invention.

### **Diagnostic, Prognostic, Serotyping and Mutation Assays**

5

This invention is also related to the use of BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polynucleotides and polypeptides of the invention for use as diagnostic reagents. Detection of BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polynucleotides and/or  
10 polypeptides in a eukaryote, particularly a mammal, and especially a human, will provide a diagnostic method for diagnosis of disease, staging of disease or response of an infectious organism to drugs. Eukaryotes, particularly mammals, and especially humans, particularly those infected or suspected to be infected with an organism comprising the BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 gene or  
15 protein, may be detected at the nucleic acid or amino acid level by a variety of well known techniques as well as by methods provided herein.

Polypeptides and polynucleotides for prognosis, diagnosis or other analysis may be obtained from a putatively infected and/or infected individual's bodily materials. Polynucleotides from  
20 any of these sources, particularly DNA or RNA, may be used directly for detection or may be amplified enzymatically by using PCR or any other amplification technique prior to analysis. RNA, particularly mRNA, cDNA and genomic DNA may also be used in the same ways. Using amplification, characterization of the species and strain of infectious or resident organism present in an individual, may be made by an analysis of the genotype of a selected  
25 polynucleotide of the organism. Deletions and insertions can be detected by a change in size of the amplified product in comparison to a genotype of a reference sequence selected from a related organism, preferably a different species of the same genus or a different strain of the same species. Point mutations can be identified by hybridizing amplified DNA to labeled BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071  
30 polynucleotide sequences. Perfectly or significantly matched sequences can be distinguished





It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component. Such a kit will be of use in diagnosing a disease or susceptibility to a disease, among others.

- 5 This invention also relates to the use of polynucleotides of the present invention as diagnostic reagents. Detection of a mutated form of a polynucleotide of the invention, preferable, SEQ ID NO:1,3,5,7,9,11,13,15 which is associated with a disease or pathogenicity will provide a diagnostic tool that can add to, or define, a diagnosis of a disease, a prognosis of a course of disease, a determination of a stage of disease, or a susceptibility to a disease, which results  
10 from under-expression, over-expression or altered expression of the polynucleotide. Organisms, particularly infectious organisms, carrying mutations in such polynucleotide may be detected at the polynucleotide level by a variety of techniques, such as those described elsewhere herein.
- 15 Cells from an organism carrying mutations or polymorphisms (allelic variations) in a polynucleotide and/or polypeptide of the invention may also be detected at the polynucleotide or polypeptide level by a variety of techniques, to allow for serotyping, for example. For example, RT-PCR can be used to detect mutations in the RNA. It is particularly preferred to use RT-PCR in conjunction with automated detection systems, such as, for example,  
20 GeneScan. RNA, cDNA or genomic DNA may also be used for the same purpose, PCR. As an example, PCR primers complementary to a polynucleotide encoding BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptide can be used to identify and analyze mutations.
- 25 The invention further provides primers with 1, 2, 3 or 4 nucleotides removed from the 5' and/or the 3' end. These primers may be used for, among other things, amplifying BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 DNA and/or RNA isolated from a sample derived from an individual, such as a bodily material. The primers may be used to amplify a polynucleotide isolated from an infected individual,  
30 such that the polynucleotide may then be subject to various techniques for elucidation of the

polynucleotide sequence. In this way, mutations in the polynucleotide sequence may be detected and used to diagnose and/or prognose the infection or its stage or course, or to serotype and/or classify the infectious agent.

- 5 The invention further provides a process for diagnosing disease, preferably bacterial infections, more preferably infections caused by *Neisseria meningitidis*, comprising determining from a sample derived from an individual, such as a bodily material, an increased level of expression of polynucleotide having a sequence of SEQ ID NO:1,3,5,7,9,11,13,15. Increased or decreased expression of a BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polynucleotide can be measured using any one of the methods well known in the art for the quantitation of polynucleotides, such as, for example, amplification, PCR, RT-PCR, RNase protection, Northern blotting, spectrometry and other hybridization methods.
- 10
- 15 In addition, a diagnostic assay in accordance with the invention for detecting over-expression of BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptide compared to normal control tissue samples may be used to detect the presence of an infection, for example. Assay techniques that can be used to determine levels of a BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptide, in a sample derived from a host, such as a bodily material, are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis, antibody sandwich assays, antibody detection and ELISA assays.
- 20
- 25 The polynucleotides of the invention may be used as components of polynucleotide arrays, preferably high density arrays or grids. These high density arrays are particularly useful for diagnostic and prognostic purposes. For example, a set of spots each comprising a different gene, and further comprising a polynucleotide or polynucleotides of the invention, may be used for probing, such as using hybridization or nucleic acid amplification, using a probe obtained or derived from a bodily sample, to determine the
- 30

presence of a particular polynucleotide sequence or related sequence in an individual. Such a presence may indicate the presence of a pathogen, particularly *Neisseria meningitidis*, and may be useful in diagnosing and/or prognosing disease or a course of disease. A grid comprising a number of variants of the polynucleotide sequence of SEQ ID NO:1,3,5,7,9,11,13,15 are preferred. Also preferred is a grid comprising a number of variants of a polynucleotide sequence encoding the polypeptide sequence of SEQ ID NO:2,4,6,8,10,12,14,16.

### Antibodies

10

The polypeptides and polynucleotides of the invention or variants thereof, or cells expressing the same can be used as immunogens to produce antibodies immunospecific for such polypeptides or polynucleotides respectively.

15 In certain preferred embodiments of the invention there are provided antibodies against BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptides or polynucleotides.

Antibodies generated against the polypeptides or polynucleotides of the invention can be obtained by administering the polypeptides and/or polynucleotides of the invention, or epitope-bearing fragments of either or both, analogues of either or both, or cells expressing either or both, to an animal, preferably a nonhuman, using routine protocols. For preparation of monoclonal antibodies, any technique known in the art that provides antibodies produced by continuous cell line cultures can be used. Examples include various techniques, such as those in Kohler, G. and Milstein, C., *Nature* 256: 495-497 (1975); Kozbor *et al.*, *Immunology Today* 4: 72 (1983); Cole *et al.*, pg. 77-96 in *MONOCLONAL ANTIBODIES AND CANCER THERAPY*, Alan R. Liss, Inc. (1985).

Techniques for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to polypeptides or polynucleotides of this

invention. Also, transgenic mice, or other organisms or animals, such as other mammals, may be used to express humanized antibodies immunospecific to the polypeptides or polynucleotides of the invention.

- 5 Alternatively, phage display technology may be utilized to select antibody genes with binding activities towards a polypeptide of the invention either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing anti- BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 or from naive libraries (McCafferty, *et al.*, (1990), *Nature* 348, 552-554; Marks, *et al.*, (1992) 10 *Biotechnology* 10, 779-783). The affinity of these antibodies can also be improved by, for example, chain shuffling (Clackson *et al.*, (1991) *Nature* 352: 628).

The above-described antibodies may be employed to isolate or to identify clones expressing the polypeptides or polynucleotides of the invention to purify the polypeptides or 15 polynucleotides by, for example, affinity chromatography.

Thus, among others, antibodies against BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 -polypeptide or BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 -polynucleotide may 20 be employed to treat infections, particularly bacterial infections.

Polypeptide variants include antigenically, epitopically or immunologically equivalent variants form a particular aspect of this invention.

- 25 Preferably, the antibody or variant thereof is modified to make it less immunogenic in the individual. For example, if the individual is human the antibody may most preferably be "humanized," where the complementarity determining region or regions of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in Jones *et al.* (1986), *Nature* 321, 522-525 or Tempest *et al.*, (1991) 30 *Biotechnology* 9, 266-273.

## Antagonists and Agonists - Assays and Molecules

Polypeptides and polynucleotides of the invention may also be used to assess the binding of small molecule substrates and ligands in, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. These substrates and ligands may be natural substrates and ligands or may be structural or functional mimetics. See, *e.g.*, Coligan *et al.*, *Current Protocols in Immunology* 1(2): Chapter 5 (1991).

The screening methods may simply measure the binding of a candidate compound to the polypeptide or polynucleotide, or to cells or membranes bearing the polypeptide or polynucleotide, or a fusion protein of the polypeptide by means of a label directly or indirectly associated with the candidate compound. Alternatively, the screening method may involve competition with a labeled competitor. Further, these screening methods may test whether the candidate compound results in a signal generated by activation or inhibition of the polypeptide or polynucleotide, using detection systems appropriate to the cells comprising the polypeptide or polynucleotide. Inhibitors of activation are generally assayed in the presence of a known agonist and the effect on activation by the agonist by the presence of the candidate compound is observed. Constitutively active polypeptide and/or constitutively expressed polypeptides and polynucleotides may be employed in screening methods for inverse agonists or inhibitors, in the absence of an agonist or inhibitor, by testing whether the candidate compound results in inhibition of activation of the polypeptide or polynucleotide, as the case may be. Further, the screening methods may simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide or polynucleotide of the present invention, to form a mixture, measuring BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptide and/or polynucleotide activity in the mixture, and comparing the BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptide and/or polynucleotide activity of the mixture to a standard. Fusion proteins, such as those made from Fc portion and BASB051, BASB057, BASB060, BASB061,

BASB063, BASB065, BASB066 or BASB071 polypeptide, as hereinbefore described, can also be used for high-throughput screening assays to identify antagonists of the polypeptide of the present invention, as well as of phylogenetically and and/or functionally related polypeptides (see D. Bennett *et al.*, J Mol Recognition, 8:52-58 (1995); and K. Johanson *et al.*, J Biol Chem, 270(16):9459-9471 (1995)).

The polynucleotides, polypeptides and antibodies that bind to and/or interact with a polypeptide of the present invention may also be used to configure screening methods for detecting the effect of added compounds on the production of mRNA and/or polypeptide in cells. For example, an ELISA assay may be constructed for measuring secreted or cell associated levels of polypeptide using monoclonal and polyclonal antibodies by standard methods known in the art. This can be used to discover agents which may inhibit or enhance the production of polypeptide (also called antagonist or agonist, respectively) from suitably manipulated cells or tissues.

The invention also provides a method of screening compounds to identify those which enhance (agonist) or block (antagonist) the action of BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptides or polynucleotides, particularly those compounds that are bacteristatic and/or bactericidal. The method of screening may involve high-throughput techniques. For example, to screen for agonists or antagonists, a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, comprising BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptide and a labeled substrate or ligand of such polypeptide is incubated in the absence or the presence of a candidate molecule that may be a BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 agonist or antagonist. The ability of the candidate molecule to agonize or antagonize the BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptide is reflected in decreased binding of the labeled ligand or decreased production of product from such substrate. Molecules that bind gratuitously, *i.e.*, without inducing the effects of BASB051, BASB057, BASB060,

BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptide are most likely to be good antagonists. Molecules that bind well and, as the case may be, increase the rate of product production from substrate, increase signal transduction, or increase chemical channel activity are agonists. Detection of the rate or level of, as the case may be, production of product from substrate, signal transduction, or chemical channel activity may be enhanced by using a reporter system. Reporter systems that may be useful in this regard include but are not limited to colorimetric, labeled substrate converted into product, a reporter gene that is responsive to changes in BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polynucleotide or polypeptide activity, and binding assays known in the art.

Another example of an assay for BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 agonists is a competitive assay that combines BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 and a potential agonist with BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 -binding molecules, recombinant BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 can be labeled, such as by radioactivity or a colorimetric compound, such that the number of BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 molecules bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include, among others, small organic molecules, peptides, polypeptides and antibodies that bind to a polynucleotide and/or polypeptide of the invention and thereby inhibit or extinguish its activity or expression. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds the same sites on a binding molecule, such as a binding molecule, without inducing BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071

-induced activities, thereby preventing the action or expression of BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptides and/or polynucleotides by excluding BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptides and/or polynucleotides from binding.

5

Potential antagonists include a small molecule that binds to and occupies the binding site of the polypeptide thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules. Other potential antagonists include antisense molecules (see Okano, *J. Neurochem.* 56: 560 (1991); *OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION*, CRC Press, Boca Raton, FL (1988), for a description of these molecules). Preferred potential antagonists include compounds related to and variants of BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071.

10

15

In a further aspect, the present invention relates to genetically engineered soluble fusion proteins comprising a polypeptide of the present invention, or a fragment thereof, and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE). Preferred as an immunoglobulin is the constant part of the heavy chain of human IgG, particularly IgG1, where fusion takes place at the hinge region. In a particular embodiment, the Fc part can be removed simply by incorporation of a cleavage sequence which can be cleaved with blood clotting factor Xa. Furthermore, this invention relates to processes for the preparation of these fusion proteins by genetic engineering, and to the use thereof for drug screening, diagnosis and therapy. A further aspect of the invention also relates to polynucleotides encoding such fusion proteins. Examples of fusion protein technology can be found in International Patent Application Nos. WO94/29458 and WO94/22914.

20

25

30

Each of the polynucleotide sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein, upon expression, can be



used as a target for the screening of antibacterial drugs. Additionally, the polynucleotide sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

5

The invention also provides the use of the polypeptide, polynucleotide, agonist or antagonist of the invention to interfere with the initial physical interaction between a pathogen or pathogens and a eukaryotic, preferably mammalian, host responsible for sequelae of infection. In particular, the molecules of the invention may be used: in the

10

prevention of adhesion of bacteria, in particular gram positive and/or gram negative bacteria, to eukaryotic, preferably mammalian, extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in wounds; to block bacterial adhesion between eukaryotic, preferably mammalian, extracellular matrix proteins and bacterial BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 proteins

15

that mediate tissue damage and/or; to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

In accordance with yet another aspect of the invention, there are provided BASB051,

20

BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 agonists and antagonists, preferably bacteristatic or bactericidal agonists and antagonists.

The antagonists and agonists of the invention may be employed, for instance, to prevent, inhibit and/or treat diseases.

25

In a further aspect, the present invention relates to mimotopes of the polypeptide of the invention. A mimotope is a peptide sequence, sufficiently similar to the native peptide (sequentially or structurally), which is capable of being recognised by antibodies which recognise the native peptide; or is capable of raising antibodies which recognise the

30

native peptide when coupled to a suitable carrier.

Peptide mimotopes may be designed for a particular purpose by addition, deletion or substitution of elected amino acids. Thus, the peptides may be modified for the purposes of ease of conjugation to a protein carrier. For example, it may be desirable for some chemical conjugation methods to include a terminal cysteine. In addition it may be desirable for peptides conjugated to a protein carrier to include a hydrophobic terminus distal from the conjugated terminus of the peptide, such that the free unconjugated end of the peptide remains associated with the surface of the carrier protein. Thereby presenting the peptide in a conformation which most closely resembles that of the peptide as found in the context of the whole native molecule. For example, the peptides may be altered to have an N-terminal cysteine and a C-terminal hydrophobic amidated tail. Alternatively, the addition or substitution of a D-stereoisomer form of one or more of the amino acids may be performed to create a beneficial derivative, for example to enhance stability of the peptide.

Alternatively, peptide mimotopes may be identified using antibodies which are capable themselves of binding to the polypeptides of the present invention using techniques such as phage display technology (EP 0 552 267 B1). This technique, generates a large number of peptide sequences which mimic the structure of the native peptides and are, therefore, capable of binding to anti-native peptide antibodies, but may not necessarily themselves share significant sequence homology to the native polypeptide.

### Vaccines

Another aspect of the invention relates to a method for inducing an immunological response in an individual, particularly a mammal, preferably humans, which comprises inoculating the individual with BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polynucleotide and/or polypeptide, or a fragment or variant thereof, adequate to produce antibody and/ or T cell immune response to protect said individual from infection, particularly bacterial infection and most particularly

*Neisseria meningitidis* infection. Also provided are methods whereby such immunological response slows bacterial replication.

Yet another aspect of the invention relates to a method of inducing immunological response  
 5 in an individual which comprises delivering to such individual a nucleic acid vector, sequence or ribozyme to direct expression of BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polynucleotide and/or polypeptide, or a fragment or a variant thereof, for expressing BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polynucleotide and/or polypeptide, or a  
 10 fragment or a variant thereof *in vivo* in order to induce an immunological response, such as, to produce antibody and/ or T cell immune response, including, for example, cytokine-producing T cells or cytotoxic T cells, to protect said individual, preferably a human, from disease, whether that disease is already established within the individual or not. One example of administering the gene is by accelerating it into the desired cells as a coating on  
 15 particles or otherwise. Such nucleic acid vector may comprise DNA, RNA, a ribozyme, a modified nucleic acid, a DNA/RNA hybrid, a DNA-protein complex or an RNA-protein complex.

A further aspect of the invention relates to an immunological composition that when  
 20 introduced into an individual, preferably a human, capable of having induced within it an immunological response, induces an immunological response in such individual to a BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polynucleotide and/or polypeptide encoded therefrom, wherein the composition comprises a recombinant BASB051, BASB057, BASB060, BASB061, BASB063, BASB065,  
 25 BASB066 or BASB071 polynucleotide and/or polypeptide encoded therefrom and/or comprises DNA and/or RNA which encodes and expresses an antigen of said BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polynucleotide, polypeptide encoded therefrom, or other polypeptide of the invention. The immunological response may be used therapeutically or prophylactically and may take the

form of antibody immunity and/or cellular immunity, such as cellular immunity arising from CTL or CD4+ T cells.

A BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptide or a fragment thereof may be fused with co-protein or chemical moiety which may or may not by itself produce antibodies, but which is capable of stabilizing the first protein and producing a fused or modified protein which will have antigenic and/or immunogenic properties, and preferably protective properties. Thus fused recombinant protein, preferably further comprises an antigenic co-protein, such as lipoprotein D from *Haemophilus influenzae*, Glutathione-S-transferase (GST) or beta-galactosidase, or any other relatively large co-protein which solubilizes the protein and facilitates production and purification thereof. Moreover, the co-protein may act as an adjuvant in the sense of providing a generalized stimulation of the immune system of the organism receiving the protein. The co-protein may be attached to either the amino- or carboxy-terminus of the first protein.

In a vaccine composition according to the invention, a BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptide and/or polynucleotide, or a fragment, or a mimotope, or a variant thereof may be present in a vector, such as the live recombinant vectors described above for example live bacterial vectors.

Also suitable are non-live vectors for the BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptide, for example bacterial outer-membrane vesicles or “blebs”. OM blebs are derived from the outer membrane of the two-layer membrane of Gram-negative bacteria and have been documented in many Gram-negative bacteria (Zhou, L *et al.* 1998. *FEMS Microbiol. Lett.* 163:223-228) including *C. trachomatis* and *C. psittaci*. A non-exhaustive list of bacterial pathogens reported to produce blebs also includes: *Bordetella pertussis*, *Borrelia burgdorferi*, *Brucella melitensis*, *Brucella ovis*, *Escherichia coli*, *Haemophilus influenza*, *Legionella pneumophila*.

*Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pseudomonas aeruginosa* and *Yersinia enterocolitica*.

Blebs have the advantage of providing outer-membrane proteins in their native  
 5 conformation and are thus particularly useful for vaccines. Blebs can also be improved for  
 vaccine use by engineering the bacterium so as to modify the expression of one or more  
 molecules at the outer membrane. Thus for example the expression of a desired  
 immunogenic protein at the outer membrane, such as the BASB051, BASB057, BASB060,  
 BASB061, BASB063, BASB065, BASB066 or BASB071 polypeptide, can be introduced or  
 10 upregulated (e.g. by altering the promoter). Instead or in addition, the expression of outer-  
 membrane molecules which are either not relevant (e.g. unprotective antigens or  
 immunodominant but variable proteins) or detrimental (e.g. toxic molecules such as LPS,  
 or potential inducers of an autoimmune response) can be downregulated. These approaches  
 are discussed in more detail below.

15 The non-coding flanking regions of the BASB051, BASB057, BASB060, BASB061,  
 BASB063, BASB065, BASB066 or BASB071 gene contains regulatory elements important  
 in the expression of the gene. This regulation takes place both at the transcriptional and  
 translational level. The sequence of these regions, either upstream or downstream of the  
 20 open reading frame of the gene, can be obtained by DNA sequencing. This sequence  
 information allows the determination of potential regulatory motifs such as the different  
 promoter elements, terminator sequences, inducible sequence elements, repressors,  
 elements responsible for phase variation, the shine-dalgarno sequence, regions with  
 potential secondary structure involved in regulation, as well as other types of regulatory  
 25 motifs or sequences.

This sequence information allows the modulation of the natural expression of the  
 BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071  
 gene. The upregulation of the gene expression may be accomplished by altering the  
 30 promoter, the shine-dalgarno sequence, potential repressor or operator elements, or any

other elements involved. Likewise, downregulation of expression can be achieved by similar types of modification. Alternatively, by changing phase variation sequences, the expression of the gene can be put under phase variation control, or it may be uncoupled from this regulation. In another approach, the expression of the gene can be put under the control of one or more inducible elements allowing regulated expression. Examples of such regulation include, but are not limited to, induction by temperature shift, addition of inductor substrates like selected carbohydrates or their derivatives, trace elements, vitamins, co-factors, metal ions, etc.

Such modifications as described above can be introduced by several different means. The modification of sequences involved in gene expression can be carried out *in vivo* by random mutagenesis followed by selection for the desired phenotype. Another approach consists in isolating the region of interest and modifying it by random mutagenesis, or site-directed replacement, insertion or deletion mutagenesis. The modified region can then be reintroduced into the bacterial genome by homologous recombination, and the effect on gene expression can be assessed. In another approach, the sequence knowledge of the region of interest can be used to replace or delete all or part of the natural regulatory sequences. In this case, the regulatory region targeted is isolated and modified so as to contain the regulatory elements from another gene, a combination of regulatory elements from different genes, a synthetic regulatory region, or any other regulatory region, or to delete selected parts of the wild-type regulatory sequences. These modified sequences can then be reintroduced into the bacterium via homologous recombination into the genome. A non-exhaustive list of preferred promoters that could be used for up-regulation of gene expression includes the promoters *porA*, *porB*, *lbpB*, *tbpB*, *p110*, *lst*, *hpuAB* from *N. meningitidis* or *N. gonorrhoeae*; *ompCD*, *copB*, *lbpB*, *ompE*, *UspA1*; *UspA2*; *TbpB* from *M. Catarrhalis*; *p1*, *p2*, *p4*, *p5*, *p6*, *lpD*, *tbpB*, *D15*, *Hia*, *Hmw1*, *Hmw2* from *H. influenzae*.

In one example, the expression of the gene can be modulated by exchanging its promoter with a stronger promoter (through isolating the upstream sequence of the gene, in vitro modification of this sequence, and reintroduction into the genome by homologous

recombination). Upregulated expression can be obtained in both the bacterium as well as in the outer membrane vesicles shed (or made) from the bacterium.

In other examples, the described approaches can be used to generate recombinant bacterial strains with improved characteristics for vaccine applications. These can be, but are not limited to, attenuated strains, strains with increased expression of selected antigens, strains with knock-outs (or decreased expression) of genes interfering with the immune response, strains with modulated expression of immunodominant proteins, strains with modulated shedding of outer-membrane vesicles.

10

Thus, also provided by the invention is a modified upstream region of the BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 gene, which modified upstream region contains a heterologous regulatory element which alters the expression level of the BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 protein located at the outer membrane. The upstream region according to this aspect of the invention includes the sequence upstream of the BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 gene. The upstream region starts immediately upstream of the BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 or BASB071 gene and continues usually to a position no more than about 1000 bp upstream of the gene from the ATG start codon. In the case of a gene located in a polycistronic sequence (operon) the upstream region can start immediately preceding the gene of interest, or preceding the first gene in the operon. Preferably, a modified upstream region according to this aspect of the invention contains a heterologous promotor at a position between 500 and 700 bp upstream of the ATG.

25

Thus, the invention provides a BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 and BASB071 polypeptide, in a modified bacterial bleb. The invention further provides modified host cells capable of producing the non-live membrane-based bleb vectors. The invention further provides nucleic acid vectors comprising the BASB051,





5 bodily fluid, preferably the blood, of the individual; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use.

10 The vaccine formulation of the invention may also include adjuvant systems for enhancing the immunogenicity of the formulation. Preferably the adjuvant system raises preferentially a TH1 type of response.

15 An immune response may be broadly distinguished into two extreme categories, being a humoral or cell mediated immune responses (traditionally characterised by antibody and cellular effector mechanisms of protection respectively). These categories of response have been termed TH1-type responses (cell-mediated response), and TH2-type immune responses (humoral response).

20 Extreme TH1-type immune responses may be characterised by the generation of antigen specific, haplotype restricted cytotoxic T lymphocytes, and natural killer cell responses. In mice TH1-type responses are often characterised by the generation of antibodies of the IgG2a subtype, whilst in the human these correspond to IgG1 type antibodies. TH2-type immune responses are characterised by the generation of a broad range of immunoglobulin isotypes including in mice IgG1, IgA, and IgM.

25 It can be considered that the driving force behind the development of these two types of immune responses are cytokines. High levels of TH1-type cytokines tend to favour the induction of cell mediated immune responses to the given antigen, whilst high levels of TH2-type cytokines tend to favour the induction of humoral immune responses to the antigen.

The distinction of TH1 and TH2-type immune responses is not absolute. In reality an individual will support an immune response which is described as being predominantly TH1 or predominantly TH2. However, it is often convenient to consider the families of cytokines in terms of that described in murine CD4 +ve T cell clones by Mosmann and  
 5 Coffman (*Mosmann, T.R. and Coffman, R.L. (1989) TH1 and TH2 cells: different patterns of lymphokine secretion lead to different functional properties. Annual Review of Immunology, 7, p145-173*). Traditionally, TH1-type responses are associated with the production of the INF- $\gamma$  and IL-2 cytokines by T-lymphocytes. Other cytokines often directly associated with the induction of TH1-type immune responses are not produced by  
 10 T-cells, such as IL-12. In contrast, TH2- type responses are associated with the secretion of IL-4, IL-5, IL-6 and IL-13.

It is known that certain vaccine adjuvants are particularly suited to the stimulation of either TH1 or TH2 - type cytokine responses. Traditionally the best indicators of the  
 15 TH1:TH2 balance of the immune response after a vaccination or infection includes direct measurement of the production of TH1 or TH2 cytokines by T lymphocytes *in vitro* after restimulation with antigen, and/or the measurement of the IgG1:IgG2a ratio of antigen specific antibody responses.

20 Thus, a TH1-type adjuvant is one which preferentially stimulates isolated T-cell populations to produce high levels of TH1-type cytokines when re-stimulated with antigen *in vitro*, and promotes development of both CD8+ cytotoxic T lymphocytes and antigen specific immunoglobulin responses associated with TH1-type isotype.

25 Adjuvants which are capable of preferential stimulation of the TH1 cell response are described in International Patent Application No. WO 94/00153 and WO 95/17209.

3 De-O-acylated monophosphoryl lipid A (3D-MPL) is one such adjuvant. This is known from GB 2220211 (Ribi). Chemically it is a mixture of 3 De-O-acylated  
 30 monophosphoryl lipid A with 4, 5 or 6 acylated chains and is manufactured by Ribi

Immunochem, Montana. A preferred form of 3 De-O-acylated monophosphoryl lipid A is disclosed in European Patent 0 689 454 B1 (SmithKline Beecham Biologicals SA).

5 Preferably, the particles of 3D-MPL are small enough to be sterile filtered through a 0.22micron membrane (European Patent number 0 689 454).

3D-MPL will be present in the range of 10µg - 100µg preferably 25-50µg per dose wherein the antigen will typically be present in a range 2-50µg per dose.

10 Another preferred adjuvant comprises QS21, an Hplc purified non-toxic fraction derived from the bark of Quillaja Saponaria Molina. Optionally this may be admixed with 3 De-O-acylated monophosphoryl lipid A (3D-MPL), optionally together with a carrier.

The method of production of QS21 is disclosed in US patent No. 5,057,540.

15 Non-reactogenic adjuvant formulations containing QS21 have been described previously (WO 96/33739). Such formulations comprising QS21 and cholesterol have been shown to be successful TH1 stimulating adjuvants when formulated together with an antigen.

20 Further adjuvants which are preferential stimulators of TH1 cell response include immunomodulatory oligonucleotides, for example unmethylated CpG sequences as disclosed in WO 96/02555.

25 Combinations of different TH1 stimulating adjuvants, such as those mentioned hereinabove, are also contemplated as providing an adjuvant which is a preferential stimulator of TH1 cell response. For example, QS21 can be formulated together with 3D-MPL. The ratio of QS21 : 3D-MPL will typically be in the order of 1 : 10 to 10 : 1; preferably 1:5 to 5 : 1 and often substantially 1 : 1. The preferred range for optimal synergy is 2.5 : 1 to 1 : 1 3D-MPL: QS21.

Preferably a carrier is also present in the vaccine composition according to the invention. The carrier may be an oil in water emulsion, or an aluminium salt, such as aluminium phosphate or aluminium hydroxide.

5 A preferred oil-in-water emulsion comprises a metabolisable oil, such as squalene, alpha tocopherol and Tween 80. In a particularly preferred aspect the antigens in the vaccine composition according to the invention are combined with QS21 and 3D-MPL in such an emulsion. Additionally the oil in water emulsion may contain span 85 and/or lecithin and/or tricaprylin.

10

Typically for human administration QS21 and 3D-MPL will be present in a vaccine in the range of 1µg - 200µg, such as 10-100µg, preferably 10µg - 50µg per dose. Typically the oil in water will comprise from 2 to 10% squalene, from 2 to 10% alpha tocopherol and from 0.3 to 3% tween 80. Preferably the ratio of squalene: alpha tocopherol is equal to or less than 1 as this provides a more stable emulsion. Span 85 may also be present at a level of 1%. In some cases it may be advantageous that the vaccines of the present invention will further contain a stabiliser.

15

Non-toxic oil in water emulsions preferably contain a non-toxic oil, e.g. squalane or squalene, an emulsifier, e.g. Tween 80, in an aqueous carrier. The aqueous carrier may be, for example, phosphate buffered saline.

20

A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil in water emulsion is described in WO 95/17210.

25

The present invention also provides a polyvalent vaccine composition comprising a vaccine formulation of the invention in combination with other antigens, in particular antigens useful for treating cancers, autoimmune diseases and related conditions. Such a polyvalent vaccine composition may include a TH-1 inducing adjuvant as hereinbefore described.

30



Polypeptides, polynucleotides and other compounds of the invention may be employed alone or in conjunction with other compounds, such as therapeutic compounds.

5 The pharmaceutical compositions may be administered in any effective, convenient manner including, for instance, administration by topical, oral, anal, vaginal, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes among others.

In therapy or as a prophylactic, the active agent may be administered to an individual as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

10

In a further aspect, the present invention provides for pharmaceutical compositions comprising a therapeutically effective amount of a polypeptide and/or polynucleotide, such as the soluble form of a polypeptide and/or polynucleotide of the present invention, agonist or antagonist peptide or small molecule compound, in combination with a pharmaceutically  
15 acceptable carrier or excipient. Such carriers include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The invention further relates to pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention. Polypeptides, polynucleotides and other compounds of the present invention may be employed alone or in  
20 conjunction with other compounds, such as therapeutic compounds.

The composition will be adapted to the route of administration, for instance by a systemic or an oral route. Preferred forms of systemic administration include injection, typically by intravenous injection. Other injection routes, such as subcutaneous, intramuscular, or  
25 intraperitoneal, can be used. Alternative means for systemic administration include transmucosal and transdermal administration using penetrants such as bile salts or fusidic acids or other detergents. In addition, if a polypeptide or other compounds of the present invention can be formulated in an enteric or an encapsulated formulation, oral administration may also be possible. Administration of these compounds may also be topical and/or  
30 localized, in the form of salves, pastes, gels, solutions, powders and the like.

- For administration to mammals, and particularly humans, it is expected that the daily dosage level of the active agent will be from 0.01 mg/kg to 10 mg/kg, typically around 1 mg/kg. The physician in any event will determine the actual dosage which will be most suitable for an individual and will vary with the age, weight and response of the particular individual. The above dosages are exemplary of the average case. There can, of course, be individual instances where higher or lower dosage ranges are merited, and such are within the scope of this invention.
- 10 The dosage range required depends on the choice of peptide, the route of administration, the nature of the formulation, the nature of the subject's condition, and the judgment of the attending practitioner. Suitable dosages, however, are in the range of 0.1-100  $\mu$ g/kg of subject.
- 15 A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response. A suitable unit dose for vaccination is 0.5-5 microgram/kg of antigen, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks. With the indicated dose range, no adverse toxicological effects will be observed with the compounds of the invention which would preclude their
- 20 administration to suitable individuals.

- Wide variations in the needed dosage, however, are to be expected in view of the variety of compounds available and the differing efficiencies of various routes of administration. For example, oral administration would be expected to require higher dosages than administration
- 25 by intravenous injection. Variations in these dosage levels can be adjusted using standard empirical routines for optimization, as is well understood in the art.

#### **Sequence Databases, Sequences in a Tangible Medium, and Algorithms**

Polynucleotide and polypeptide sequences form a valuable information resource with which to determine their 2- and 3-dimensional structures as well as to identify further sequences of similar homology. These approaches are most easily facilitated by storing the sequence in a computer readable medium and then using the stored data in a known macromolecular structure program or to search a sequence database using well known searching tools, such as the GCG program package.

Also provided by the invention are methods for the analysis of character sequences or strings, particularly genetic sequences or encoded protein sequences. Preferred methods of sequence analysis include, for example, methods of sequence homology analysis, such as identity and similarity analysis, DNA, RNA and protein structure analysis, sequence assembly, cladistic analysis, sequence motif analysis, open reading frame determination, nucleic acid base calling, codon usage analysis, nucleic acid base trimming, and sequencing chromatogram peak analysis.

15 A computer based method is provided for performing homology identification. This method comprises the steps of: providing a first polynucleotide sequence comprising the sequence of a polynucleotide of the invention in a computer readable medium; and comparing said first polynucleotide sequence to at least one second polynucleotide or  
20 polypeptide sequence to identify homology.

A computer based method is also provided for performing homology identification, said method comprising the steps of: providing a first polypeptide sequence comprising the sequence of a polypeptide of the invention in a computer readable medium; and comparing  
25 said first polypeptide sequence to at least one second polynucleotide or polypeptide sequence to identify homology.

30 All publications and references, including but not limited to patents and patent applications, cited in this specification are herein incorporated by reference in their entirety as if each individual publication or reference were specifically and individually indicated to be



incorporated by reference herein as being fully set forth. Any patent application to which this application claims priority is also incorporated by reference herein in its entirety in the manner described above for publications and references.

## 5 DEFINITIONS

"Identity," as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as the case may be, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between  
10 polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. "Identity" can be readily calculated by known methods, including but not limited to those described in (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis*  
15 *of Sequence Data*, Part I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heine, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48: 1073 (1988). Methods to determine identity are designed to give the largest match between the sequences  
20 tested. Moreover, methods to determine identity are codified in publicly available computer programs. Computer program methods to determine identity between two sequences include, but are not limited to, the GAP program in the GCG program package (Devereux, J., et al., *Nucleic Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN (Altschul, S.F. et al., *J. Mol. Biol.* 215: 403-410 (1990), and FASTA( Pearson and Lipman  
25 *Proc. Natl. Acad. Sci. USA* 85; 2444-2448 (1988). The BLAST family of programs is publicly available from NCBI and other sources (*BLAST Manual*, Altschul, S., et al., NCBI NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215: 403-410 (1990). The well known Smith Waterman algorithm may also be used to determine identity.

30 Parameters for polypeptide sequence comparison include the following:

Algorithm: Needleman and Wunsch, J. Mol Biol. 48: 443-453 (1970)

Comparison matrix: BLOSSUM62 from Henikoff and Henikoff,

Proc. Natl. Acad. Sci. USA. 89:10915-10919 (1992)

Gap Penalty: 8

5 Gap Length Penalty: 2

A program useful with these parameters is publicly available as the "gap" program from Genetics Computer Group, Madison WI. The aforementioned parameters are the default parameters for peptide comparisons (along with no penalty for end gaps).

10 Parameters for polynucleotide comparison include the following:

Algorithm: Needleman and Wunsch, J. Mol Biol. 48: 443-453 (1970)

Comparison matrix: matches = +10, mismatch = 0

Gap Penalty: 50

Gap Length Penalty: 3

15 Available as: The "gap" program from Genetics Computer Group, Madison WI. These are the default parameters for nucleic acid comparisons.

A preferred meaning for "identity" for polynucleotides and polypeptides, as the case may be, are provided in (1) and (2) below.

20

(1) Polynucleotide embodiments further include an isolated polynucleotide comprising a polynucleotide sequence having at least a 50, 60, 70, 80, 85, 90, 95, 97 or 100% identity to the reference sequence of SEQ ID NO:1, wherein said polynucleotide sequence may be identical to the reference sequence of SEQ ID NO:1 or may include up to a certain integer

25 number of nucleotide alterations as compared to the reference sequence, wherein said alterations are selected from the group consisting of at least one nucleotide deletion, substitution, including transition and transversion, or insertion, and wherein said alterations may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among the  
30 nucleotides in the reference sequence or in one or more contiguous groups within the

reference sequence, and wherein said number of nucleotide alterations is determined by multiplying the total number of nucleotides in SEQ ID NO:1 by the integer defining the percent identity divided by 100 and then subtracting that product from said total number of nucleotides in SEQ ID NO:1, or:

5

$$n_n \leq x_n - (x_n \bullet y),$$

wherein  $n_n$  is the number of nucleotide alterations,  $x_n$  is the total number of nucleotides in SEQ ID NO:1,  $y$  is 0.50 for 50%, 0.60 for 60%, 0.70 for 70%, 0.80 for 80%, 0.85 for 85%,  
 10 0.90 for 90%, 0.95 for 95%, 0.97 for 97% or 1.00 for 100%, and  $\bullet$  is the symbol for the multiplication operator, and wherein any non-integer product of  $x_n$  and  $y$  is rounded down to the nearest integer prior to subtracting it from  $x_n$ . Alterations of a polynucleotide sequence encoding the polypeptide of SEQ ID NO:2 may create nonsense, missense or frameshift mutations in this coding sequence and thereby alter the polypeptide encoded by  
 15 the polynucleotide following such alterations.

By way of example, a polynucleotide sequence of the present invention may be identical to the reference sequence of SEQ ID NO:1, that is it may be 100% identical, or it may include up to a certain integer number of nucleic acid alterations as compared to the reference  
 20 sequence such that the percent identity is less than 100% identity. Such alterations are selected from the group consisting of at least one nucleic acid deletion, substitution, including transition and transversion, or insertion, and wherein said alterations may occur at the 5' or 3' terminal positions of the reference polynucleotide sequence or anywhere between those terminal positions, interspersed either individually among the nucleic acids  
 25 in the reference sequence or in one or more contiguous groups within the reference sequence. The number of nucleic acid alterations for a given percent identity is determined by multiplying the total number of nucleic acids in SEQ ID NO:1 by the integer defining the percent identity divided by 100 and then subtracting that product from said total number of nucleic acids in SEQ ID NO:1, or:

30

$$\mathbf{n}_n \leq \mathbf{x}_n - (\mathbf{x}_n \bullet \mathbf{y}),$$

wherein  $\mathbf{n}_n$  is the number of nucleic acid alterations,  $\mathbf{x}_n$  is the total number of nucleic acids in SEQ ID NO:1,  $\mathbf{y}$  is, for instance 0.70 for 70%, 0.80 for 80%, 0.85 for 85% etc.,  $\bullet$  is the symbol for the multiplication operator, and wherein any non-integer product of  $\mathbf{x}_n$  and  $\mathbf{y}$  is rounded down to the nearest integer prior to subtracting it from  $\mathbf{x}_n$ .

(2) Polypeptide embodiments further include an isolated polypeptide comprising a polypeptide having at least a 50, 60, 70, 80, 85, 90, 95, 97 or 100% identity to a polypeptide reference sequence of SEQ ID NO:2, wherein said polypeptide sequence may be identical to the reference sequence of SEQ ID NO:2 or may include up to a certain integer number of amino acid alterations as compared to the reference sequence, wherein said alterations are selected from the group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion, and wherein said alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence, and wherein said number of amino acid alterations is determined by multiplying the total number of amino acids in SEQ ID NO:2 by the integer defining the percent identity divided by 100 and then subtracting that product from said total number of amino acids in SEQ ID NO:2, or:

$$\mathbf{n}_a \leq \mathbf{x}_a - (\mathbf{x}_a \bullet \mathbf{y}),$$

25 wherein  $\mathbf{n}_a$  is the number of amino acid alterations,  $\mathbf{x}_a$  is the total number of amino acids in SEQ ID NO:2,  $\mathbf{y}$  is 0.50 for 50%, 0.60 for 60%, 0.70 for 70%, 0.80 for 80%, 0.85 for 85%, 0.90 for 90%, 0.95 for 95%, 0.97 for 97% or 1.00 for 100%, and  $\bullet$  is the symbol for the multiplication operator, and wherein any non-integer product of  $\mathbf{x}_a$  and  $\mathbf{y}$  is rounded down to the nearest integer prior to subtracting it from  $\mathbf{x}_a$ .

By way of example, a polypeptide sequence of the present invention may be identical to the reference sequence of SEQ ID NO:2, that is it may be 100% identical, or it may include up to a certain integer number of amino acid alterations as compared to the reference sequence such that the percent identity is less than 100% identity. Such alterations are selected from the group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion, and wherein said alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence. The number of amino acid alterations for a given % identity is determined by multiplying the total number of amino acids in SEQ ID NO:2 by the integer defining the percent identity divided by 100 and then subtracting that product from said total number of amino acids in SEQ ID NO:2, or:

$$n_a \leq x_a - (x_a \bullet y),$$

wherein  $n_a$  is the number of amino acid alterations,  $x_a$  is the total number of amino acids in SEQ ID NO:2,  $y$  is, for instance 0.70 for 70%, 0.80 for 80%, 0.85 for 85% etc., and  $\bullet$  is the symbol for the multiplication operator, and wherein any non-integer product of  $x_a$  and  $y$  is rounded down to the nearest integer prior to subtracting it from  $x_a$ .

"Individual(s)," when used herein with reference to an organism, means a multicellular eukaryote, including, but not limited to a metazoan, a mammal, an ovid, a bovid, a simian, a primate, and a human.

"Isolated" means altered "by the hand of man" from its natural state, *i.e.*, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living organism is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural

state is "isolated", as the term is employed herein. Moreover, a polynucleotide or polypeptide that is introduced into an organism by transformation, genetic manipulation or by any other recombinant method is "isolated" even if it is still present in said organism, which organism may be living or non-living.

5

"Polynucleotide(s)" generally refers to any polyribonucleotide or polydeoxyribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA including single and double-stranded regions.

10 "Variant" refers to a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid  
15 sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and  
20 reference polypeptide may differ in amino acid sequence by one or more substitutions, additions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides  
25 and polypeptides may be made by mutagenesis techniques or by direct synthesis.

"Disease(s)" means any disease caused by or related to infection by a bacteria, including , for example, upper respiratory tract infection, invasive bacterial diseases, such as bacteremia and meningitis.

## EXAMPLES

The examples below are carried out using standard techniques, which are well known and routine to those of skill in the art, except where otherwise described in detail. The examples  
5 are illustrative, but do not limit the invention.

### Example 1

### **The BASB051 gene in *N.meningitidis* strain ATCC 13090.**

10

The BASB051 gene of *N. meningitidis* strain ATCC 13090 is shown in SEQ ID NO:1. The translation of the BASB051 polynucleotide sequence, shown in SEQ ID NO:2, shows significant similarity to *Neisseria gonorrhoeae* ComL lipoprotein. The BASB051 polypeptide contains a leader sequence characteristic of a lipoprotein signal sequence.

15

### Example 2

### **The BASB057 gene in *N.meningitidis* strain ATCC 13090.**

20 The BASB057 gene of *N. meningitidis* strain ATCC 13090 is shown in SEQ ID NO:3. The translation of the BASB057 polynucleotide sequence, shown in SEQ ID NO:4, shows significant similarity to *Neisseria gonorrhoeae* MtrE outer membrane lipoprotein. The BASB057 polypeptide contains a leader sequence characteristic of a lipoprotein signal sequence.

25

### Example 3

### **The BASB060 gene in *N.meningitidis* strain ATCC 13090.**

The BASB060 gene of *N. meningitidis* strain ATCC 13090 is shown in SEQ ID NO:5.  
The translation of the BASB060 polynucleotide sequence, shown in SEQ ID NO:6,  
shows no significant similarity to any known protein. However, the BASB060  
polypeptide contains a leader sequence which is characteristic of a lipoprotein signal  
sequence and has the characteristics of an outer membrane lipoprotein.

#### **Example 4**

##### **The BASB061 gene in *N.meningitidis* strain ATCC 13090.**

The BASB061 gene of *N. meningitidis* strain ATCC 13090 is shown in SEQ ID NO:7.  
The translation of the BASB061 polynucleotide sequence, shown in SEQ ID NO:8,  
shows significant similarity to *Neisseria meningitidis* mlp gene product. The BASB061  
polypeptide contains a leader sequence which is characteristic of a lipoprotein signal  
sequence and has the characteristics of an outer membrane lipoprotein.

#### **Example 5**

##### **The BASB063 gene in *N.meningitidis* strain ATCC 13090.**

The BASB063 gene of *N. meningitidis* strain ATCC 13090 is shown in SEQ ID NO:9.  
The translation of the BASB063 polynucleotide sequence, shown in SEQ ID NO:10,  
shows significant similarity to any known protein. However, the BASB063 polypeptide  
does contain a leader sequence which is characteristic of a lipoprotein signal sequence  
and has the characteristics of an outer membrane lipoprotein.

#### **Example 6**

##### **The BASB065 gene in *N.meningitidis* strain ATCC 13090.**



The BASB065 gene of *N. meningitidis* strain ATCC 13090 is shown in SEQ ID NO:11. The translation of the BASB065 polynucleotide sequence, shown in SEQ ID NO:12, shows significant similarity to any known protein. However, the BASB065 polypeptide does contain a leader sequence which is characteristic of a lipoprotein signal sequence and has the characteristics of an outer membrane lipoprotein.

#### Example 7

##### The BASB066 gene in *N.meningitidis* strain ATCC 13090.

The BASB066 gene of *N. meningitidis* strain ATCC 13090 is shown in SEQ ID NO:13. The translation of the BASB066 polynucleotide sequence, shown in SEQ ID NO:14, shows significant similarity to *Neisseria meningitidis* CtrA protein. The BASB066 polypeptide contains a leader sequence which has the characteristics of a lipoprotein signal sequence and has the characteristics of a protein located in the outer membrane.

#### Example 8

##### The BASB071 gene in *N.meningitidis* strain ATCC 13090.

The BASB071 gene of *N. meningitidis* strain ATCC 13090 is shown in SEQ ID NO:15. The translation of the BASB071 polynucleotide sequence, shown in SEQ ID NO:16, shows significant similarity to *Neisseria gonorrhoeae* HisJ protein. The BASB071 polypeptide is contains a leader sequence which has the characteristics of a lipoprotein signal sequence.

## Polynucleotide and Polypeptide Sequences

### SEQ ID NO:1

*Neisseria meningitidis* BASB051 polynucleotide sequence from strain ATCC 13090

5 ATGAAAAAATTCTTTTAACGGTTTCATTAGGTTTGGCACTGAGTGCCCTGTGCCACTCAA  
GGTACGGTCGATAAAGATGCTCAGATTACCCAAGATTGGAGTGTGGAGAAGCTCTATGCC  
GAAGCCCAGGACGAATTGAACAGCAGCAATTATACGCGGGCTGTCAAGTTATACGAAATC  
TTGGAATCGCGCTTCCCCACCAGCCGCCATGCCCCGGAATCCCAACTGGATACCGCATAC  
GCCTATTATAAAGACGATGAAAAAGACAAGGCTCTGGCGGCAATCGAACGCTTCCGCCGC  
10 CTCCATCCGCAGCATCCGAATATGGATTACGCGCTGTATCTGCGCGGCTTGGTGCTGTTT  
AACGAAGACCAGTCCTTCTTGAACAAACTGGCCTCGCAAGACTGGTCCGACCGCGACCCG  
AAAGCCAACCGCGAAGTAACCCAGGCGTTTGCGGAACCTCGTCCAACGCTTCCCCAACAGC  
AAATACGCGCGCGATGCGACCGCACGCATGGTCAAACCTGGTTCGATGCACTGGGCGGCAAT  
GAAATGTTCGGTGGCGCTACTACATGAAACGCGCGCATATATCGCCGCCGCCAACCGC  
15 GCCCCAAAAATTATCGGCAGCTACCAAAATACACGCTATGTGGAAGAATCGCTCGCCATC  
TTGGAACCTTGCTACCAAAACTCGGCAAAACACAGCTTGCCGCCGATACGCGCGCGTG  
TTGGAACCAACTTCCCGAAAAGCCGTTTTTGACGCACGCTTGGCAGCCCGACGATATG  
CCTTGGTGGCGTTACTGGCATTAA

### 20 SEQ ID NO:2

*Neisseria meningitidis* BASB051 polypeptide sequence deduced from the polynucleotide sequence of SEQ ID NO:1

25 MKKILLTVSLGLALSACATQGTVDKDAQITQDWSVEKLYAEAQDELNSSNYTRAVKLYEI  
LESRFPTSRHARQSOLDTAYAYYKDDEKDKALAAIERFRRLHPQHNPMDYALYLRGLVLF  
NEDQSFLNKLASQDWSDRDPKANREVTQAFABLVQRFPNKYAADATARMVKLVLDALGGN  
EMSVARYYMKRGAYIAAANRAQKIIGSYQNTRYVEESLAILELAYQKLGKPQLAADTRRV  
LETNFPKSPFLTHAWQPDDMPWRYWH

### SEQ ID NO:3

30 *Neisseria meningitidis* BASB057 polynucleotide sequence from strain ATCC 13090

ATGGATACTACATTGAAAACACCTTGACTTCTGTTGCAGCAGCCTTCGCATTATCCGCC  
TGCACCATGATTCCCCAATACGAGCAGCCCAAAGTCGAAGTTGCCGAAACGTTTAAAAAC  
GATACCGCCGACAGCGGCATCCGTGCGGTGCGATTAGGTTGGCATGACTATTTTGCCGAC  
CCGCGCCTGCAAAAGCTGATCGACATCGCACTCGAGCGCAATACCAGTTTGCGTACCGCC  
35 GTATTGAACAGCGAAATCTACCGCAACAATACATGATTGAGCGCAACAACCTCCTGCCC  
ACGCTTGCCGCCAATGCGAACGGCTCGCGCCAAGGCAGCTTGAGCGCGGCAATGTCAGC  
AGCAGCTACAATGTCGGACTGGGTGCGGCATCTTACGAACTCGACCTGTTTCGGACGCGTC  
CGCAGCAGCAGCGAAGCAGCACTGCAAGGCTATTTTGCAAGTGTGCGCAACCGCGATGCG  
GCACATTTGAGCCTGATTGCCACCGTTGCCAAAGCCTATTTCAACGAACGTTATGCCGAA  
40 GAAGCGATGTCTTTGGCGCAGCGTGTGTTTGAACACGCGCGAGGAAACCTACAAGCTGTCC  
GAATTACGTTACAAGGCAGGCGTGATTTCCGCCGTGCGCCTACGTGAGCAGGAAGCCCTG  
ATCGAATCTGCCAAAGCCGATTATGCCCATGCCGCGCGCAGCCGCAACAGGCGCGCAAT  
GCCTTGGAACCTTGATTAACCAACCGATACCCGAAGACCTGCCTGCCGGTTTGCCGCTG  
GACAAGCAGTTTTTTGTTGAAAACTGCCGCGCGGTTTGAGTTCCGAAGTATTGCTCGAC  
45 CGTCCCGATATCCGTGCTGCCGAACACGCGCTCAAACAGGCAAACGCCAATATCGGTGCG  
GCACGCGCCGCTTTTTCCCATCCATCCGCCTGACCGGAACCGTCGGTACGGGTTCTGCC

WO 00/42191

PCT/EP00/00135

GAATTGGGTGGGTTGTTCAAAAAGCGGCACGGGCGTTTGGTCGTTTCGCGCCGTCTATTACC  
CTGCCGATTTTTACCTGGGGTACGAACAAAGCCAACCTTGATGTAGCCAAGCTGCGCCAA  
CAGGCACAAATCGTTGCCTATGAAGCCGCGCTCCAATCCGCATTTCAAGACGTGGCAAAC  
GCATTGGCGGCGCGCGAGCAGCTGGATAAAGCCTATGACGCTTTAAGCAAACAAAGCCGC  
5 GCCTCTAAAGAGGCGTTGCGCTTGGTCGGCCTGCGTTACAAGCACGGCGTATCCGGCGCG  
CTCGACTTGCTCGATGCGGAACGCAGCAGCTATGCGGCGGAGGGTGCGGCTTTGTCTGGCA  
CAACTGACCCGCGCCGAAAACCTTGCCGATTTGTACAAGGCACTCGGCGGCGGATTGAAA  
CGGGATACCCAAACCGACAAATAA

#### 10 SEQ ID NO:4

*Neisseria meningitidis* BASB057 polypeptide sequence deduced from the polynucleotide sequence of SEQ ID NO:3

MDTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFKNDTADSGIRAVDLGWHDYFAD  
PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANGSRQGSLSGGNVS  
15 SSYNVGLGAASYELDLFGRVRSSEALQGYFASVANRDAHLSLIATVAKAYFNERYAE  
EAMSLAQRVLKTRREETYKLSELYKAGVISAVALRQQEALIESAKADYAHAARSREQARN  
ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA  
ARAAFFPSIRLTGTGTGSAELGGLFKSGTGVWSFAPSITLPIFTWGTNKANLDVAKLRQ  
QAQIVAYEAAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSGA  
20 LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDK

#### SEQ ID NO:5

*Neisseria meningitidis* BASB060 polynucleotide sequence from strain ATCC 13090

25 ATGAAAAAACTTCTAATGATAACCCCTACCGGTATGCTTGCAGCTTGTGCAACAGGTGTC  
AATGTCGGCCGCTTGATGGTTGAAATGCCGCAGGGAGAACGTTCTGTCTGTTGTGCAAGTT  
CCCGCGACAAATAACCCGCTTTCCGATACGGTAGCTGTCGGAATGATTAAACATCCGGT  
TCGCCTTCGGCATCAAATATGATTGAAATGCTCGGCGCGGACAATATCAACGTCGGCGTG  
GTGGGAAGCAGCCAAATGCTTAATAAGGCGACCGCACTTTATTCTTTAAACCATGCAAAG  
30 AAAGTCGGAAATAATGTCTAGTGTATATGATGGGCGACAGCGAAAGTGACAAGGCCGAT  
TTGGAAAACGCGGCAAATGCCAAAAATATCAAATTGCATTATTTCTTTAACCAAAAATAA

#### SEQ ID NO:6

35 *Neisseria meningitidis* BASB060 polypeptide sequence deduced from the polynucleotide sequence of SEQ ID NO:5

MKKLLMITLTGMLAACATGVNVGRLMVEMPQERSVVVQVPATNNPLSDTVAVGMIKTSG  
SPSASNMIEMLGADNINVGVSQMLNKKATALYSLNHAKKVGNNVSVYMMGDSESDKAD  
LENAANAKNIKLHYFFNQK

#### 40 SEQ ID NO:7

*Neisseria meningitidis* BASB061 polynucleotide sequence from strain ATCC 13090

ATGAAAATCAAACAAATCGTCAAACCGGGCTTGGCAGTATTGGCGGCGGGCGTTCTGTCT  
GCCTGCGCAACCAAAAGCAACGTCAAAGCCGACGGAACGACCGACAATCCGGTTTCCCG  
AAACCTATTCCGTAACGCTCGACAACAATCGCGGTACATTCCCGACCTATGACGAATTG



WO 00/42191

PCT/EP00/00135

5 CCTGTTTCCCGCAATATTTCAGGATATGCGGCCCGAACCGCAGGCAGAGGCAGGTAGTTCG  
GACGCTATTCCCTATCCCGTTCCCACTCTGCAAGACCGTTTGGATTATCTGGAAGGCACA  
CTCGTCCGCCTGTGCAACGAAGTGGAACCTTAAACGGCAAAGTCAAAGCACTGGAGCAT  
GCGAAACACACCCCTTCCGGTAGGGCATACTCCAAAACTCGACGACCGCAAGTTGAAA  
10 GAGCATTACCTCAATACCGAAGGCGGCAGCGCATCCGCACATACCGTCGAAACCGCACAA  
AACCTCTACAATCAGGCACTCAAACACTATAAAAGCGGCAGGTTTTCTGCCGCAGCCGCC  
CTGTTGAAAGGCGCGGACGGAGGCGACGGCGGCAGCATCGCGCAACGCAGTATGTACCTG  
TTGCTGCAAAGCAGGGCGCGTATGGGCAACTGCGAATCCGTCATCGAAATCGGAGGGCGT  
TACGCCAACCGTTTCAAAGACAGCCCAACCGCGCCCGAAGCCATGTTCAAATCGGCGAA  
15 TGCCAATACAGGTTGCAGCAGAAAGACATTGCAAGGGCAACTTGGCGCAGCCTGATACAG  
GCTTACCCGAGCAGCCCGGCGGCAAAACGCGCCCGCAGCCGTACGCAAACGATAG

## SEQ ID NO:12

15 *Neisseria meningitidis* BASB065 polypeptide sequence deduced from the polynucleotide  
sequence of SEQ ID NO:11

MKTKLPLFIIWLSVSAACSSPVSRIQDMRPEPQAEAGSSDAIPYPVPTLQDRILDYLEGT  
LVRLSNEVETLNGKVKALEHAKTHPSGRAYVQKLDRLKEHYLNTEGGSASAHTVETAQ  
NLYNQALKHYKSGRFSAAAALLKGADGGDGSIAQRSMYLLQLSRARMGNCEVIEIGGR  
YANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQAYPSSPAAKRAAAVRKR

## SEQ ID NO:13

*Neisseria meningitidis* BASB066 polynucleotide sequence from strain ATCC 13090

25 GTGTTTAAAGTGAAATTTTATATTTCGTCACGCAGTATTATTATTGTGTGGAAGTTTAAT  
GTAGGATGCTCTGCGATTCTTCATCAGGCCCCAGCGCAAAAAAATTGTCTCTTTAGGG  
CAACAATCTGAAGTTCAAATTCCTGAAGTGGAGCTGATTGATGTGAATCATACGGTTGCT  
CAGTTATTATATAAGGCTCAGATAAATCAGTCATTCAGTTTGGCGATGGTTATGCT  
TCGGCTGGTACGCTAAATATTGGTGATGTATTGGATATTATGATTTGGGAAGCGCCCG  
GCAGTATTGTTGGTGGTGGCCTTTCTTCGATGGGCTCGGGTAGTGCGCATCAAATAAG  
30 TTGCCAGAGCAGTTGGTCACGGCACGTGGTACGGTTTCTGTGCCGTTTGTGGCGATATT  
TCGGTGGTTCGTTAAACGCCTGGTCAGGTTTCAGGAAATTATTAAAGGCCGCTGAAAAAA  
ATGGCCAATCAGCCACAAGTGATGGTGCGTTTGGTGCAGAATAATGCGGCGAATGTGTCTG  
GTGATTCGTGCTGGGAATAGTGTGCGTATGCCGCTGACGGCAGCCGGTGAGCGTGTGTTG  
GATGCGGTGGCTGCGGTAGGTGGTTCAACGGCAAATGTGCAGGATACGAATGTGCAGCTG  
ACACGTGGCAATGTAGTACGAACGTGTGCCTTGGAAGATTTAGTTGCAAATCCGCGACAA  
35 AATATTTTGTGCTGCGTGCCTGATGTGGTTACCATGATTACCAATCCCTATACCTTTACG  
TCTATGGGTGCGGTGGGGAGAACACAAGAAATCGGTTTTTCAGCCAGAGGCTTATCGCTT  
TCTGAAGCCATTGGCCGTATGGGCGGTTTGCAAGATCGCCGTTCTGATGCGCGTGGTGTG  
TTTGTGTTCCGCTATACGCCATTGGTGGAAATTGCCGGCAGAACGTACAGATAAATGGATT  
GCTCAAGGTTATGGCAGTGAGGCAGAGATTCCAACGGTATATCGTGTGAATATGGCTGAT  
40 GCGCATTGCTATTTTCTATGCAGCGCTTTCCTGTGAAGAATAAAGATGTATTGTATGTG  
TCGAATGCGCCGTTGGCTGAAGTGAGAAATCTTGTGCTTTGTGTTCTCGCCGGTTACC  
AGTGGCGCGAACAGTATTAATAATTTAACTAATTAA

## SEQ ID NO:14

45 *Neisseria meningitidis* BASB066 polypeptide sequence deduced from the polynucleotide  
sequence of SEQ ID NO:13



## Deposited materials

A deposit containing a *Neisseria meningitidis* Serogroup B strain has been deposited with the American Type Culture Collection (herein "ATCC") on June 22, 1997 and assigned deposit number 13090. The deposit was described as *Neisseria meningitidis* (Albrecht and Ghon) and is a freeze-dried, 1.5-2.9 kb insert library constructed from *N. meningitidis* isolate. The deposit is described in Int. Bull. Bacteriol. Nomencl. Taxon. 8: 1-15 (1958).

The *Neisseria meningitidis* strain deposit is referred to herein as "the deposited strain" or as "the DNA of the deposited strain."

10

The deposited strain contains the full-length BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 and BASB071 genes. The sequence of the polynucleotides contained in the deposited strain, as well as the amino acid sequence of any polypeptide encoded thereby, are controlling in the event of any conflict with any description of sequences herein.

The deposit of the deposited strain has been made under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for Purposes of Patent Procedure. The strain will be irrevocably and without restriction or condition released to the public upon the issuance of a patent. The deposited strain is provided merely as convenience to those of skill in the art and is not an admission that a deposit is required for enablement, such as that required under 35 U.S.C. §112.

WO 00/42191

PCT/EP00/00135

Applicant's or agent's file reference KP/BM45348	International application No.
--	-------------------------------

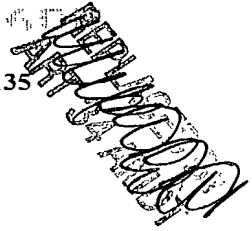
**INDICATIONS RELATING TO DEPOSITED MICROORGANISM  
OR OTHER BIOLOGICAL MATERIAL**

(PCT Rule 13bis)

A. The indications made below relate to the deposited microorganism or other biological material referred to in the description on page <u>110</u> , line <u>2-22</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution  AMERICAN TYPE CULTURE COLLECTION	
Address of depositary institution (including postal code and country) 10801 UNIVERSITY BLVD, MANASSAS, VIRGINIA 20110-2209, UNITED STATES OF AMERICA	
Date of deposit 22 June 1997 (22.06.97)	Accession Number 13090
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect of those designations where a European Patent is sought, a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European Patent or until the date on which the application has been refused or withdrawn, only by issue of such a sample to an expert nominated by the person requesting the sample.	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g. "Accession Number of Deposit")	

For receiving Office use only	For International Bureau use only
<input type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer	Authorized officer





## CLAIMS

1. An isolated polypeptide comprising an amino acid sequence which has at least 85% identity to an amino acid sequence selected from the group consisting of: SEQ ID NO:2,  
5 SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16.
2. An isolated polypeptide as claimed in claim 1 in which the amino acid sequence has at least 95% identity to the amino acid sequence selected from the group consisting of: SEQ  
10 ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16.
3. The polypeptide as claimed in claim 1 comprising the amino acid sequence selected from the group consisting of: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8,  
15 SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16.
4. An isolated polypeptide of : SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14 or SEQ ID NO:16.
- 20 5. An immunogenic fragment of the polypeptide as claimed in any one of claims 1 to 4 in which the immunogenic activity of said immunogenic fragment is substantially the same as that of the polypeptide of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14 or SEQ ID NO:16.
- 25 6. An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide that has at least 85% identity to an amino acid sequence of SEQ ID NO:2,4,6,8,10,12,14 or 16 over the entire length of SEQ ID NO:2,4,6,8,10,12,14 or 16 respectively; or a nucleotide sequence complementary to said isolated polynucleotide.



14. A host cell comprising the expression vector of claim 13 or a subcellular fraction or a membrane of said host cell expressing an isolated polypeptide comprising an amino acid sequence that has at least 85% identity to the amino acid sequence selected from the group consisting of: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16.

15. A process for producing a polypeptide comprising an amino acid sequence that has at least 85% identity to an amino acid sequence selected from the group consisting of: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16 comprising culturing a host cell of claim 14 under conditions sufficient for the production of said polypeptide and recovering the polypeptide from the culture medium.

16. A process for expressing a polynucleotide of any one of claims 6 to 12 comprising transforming a host cell with the expression vector comprising at least one of said polynucleotides and culturing said host cell under conditions sufficient for expression of any one of said polynucleotides.

17. A vaccine composition comprising an effective amount of the polypeptide of any one of claims 1 to 5 and a pharmaceutically acceptable carrier.

18. A vaccine composition comprising an effective amount of the polynucleotide of any one of claims 6 to 12 and a pharmaceutically effective carrier.

19. The vaccine composition according to either one of claims 17 or 18 wherein said composition comprises at least one other *Neisseria meningitidis* antigen.

20. An antibody immunospecific for the polypeptide or immunological fragment as claimed in any one of claims 1 to 5.

21. A method of diagnosing a *Neisseria meningitidis* infection, comprising identifying a polypeptide as claimed in any one of claims 1 to 5, or an antibody that is immunospecific for said polypeptide, present within a biological sample from an animal suspected of having  
5 such an infection.
22. Use of a composition comprising an immunologically effective amount of a polypeptide as claimed in any one of claims 1 to 5 in the preparation of a medicament for use in generating an immune response in an animal.  
10
23. Use of a composition comprising an immunologically effective amount of a polynucleotide as claimed in any one of claims 6 to 12 in the preparation of a medicament for use in generating an immune response in an animal.
- 15 24. A therapeutic composition useful in treating humans with *Neisseria meningitidis* disease comprising at least one antibody directed against the polypeptide of claims 1 to 5 and a suitable pharmaceutical carrier.

**PCT**WORLD INTELLECTUAL PROPERTY ORGANIZATION  
International Bureau

## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>7</sup> :</b> <b>C12N 15/31, C07K 14/22, A61K 39/095, C07K 16/12, G01N 33/569</b>		<b>A3</b>	<b>(11) International Publication Number:</b> <b>WO 00/42191</b> <b>(43) International Publication Date:</b> 20 July 2000 (20.07.00)																																				
<b>(21) International Application Number:</b> PCT/EP00/00135 <b>(22) International Filing Date:</b> 10 January 2000 (10.01.00) <b>(30) Priority Data:</b> <table border="0"><tr><td>9900952.4</td><td>15 January 1999 (15.01.99)</td><td>GB</td></tr><tr><td>9900838.5</td><td>15 January 1999 (15.01.99)</td><td>GB</td></tr><tr><td>9901945.7</td><td>28 January 1999 (28.01.99)</td><td>GB</td></tr><tr><td>9901948.1</td><td>28 January 1999 (28.01.99)</td><td>GB</td></tr><tr><td>9902078.6</td><td>29 January 1999 (29.01.99)</td><td>GB</td></tr><tr><td>9902088.5</td><td>29 January 1999 (29.01.99)</td><td>GB</td></tr><tr><td>9902074.5</td><td>29 January 1999 (29.01.99)</td><td>GB</td></tr><tr><td>9902879.7</td><td>9 February 1999 (09.02.99)</td><td>GB</td></tr><tr><td>9902936.5</td><td>10 February 1999 (10.02.99)</td><td>GB</td></tr><tr><td>9903978.6</td><td>20 February 1999 (20.02.99)</td><td>GB</td></tr><tr><td>9904133.7</td><td>23 February 1999 (23.02.99)</td><td>GB</td></tr><tr><td>9904404.2</td><td>25 February 1999 (25.02.99)</td><td>GB</td></tr></table> <b>(71) Applicant (for all designated States except US):</b> SMITHK-LINE BEECHAM BIOLOGICALS S.A. [BE/BE]; Rue de l'Institut 89, B-1330 Rixensart (BE). <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> RUELLE, Jean-Louis [BE/BE]; SmithKline Beecham Biologicals S.A., Rue de l'Institut 89, B-1330 Rixensart (BE). THONNARD, Joelle			9900952.4	15 January 1999 (15.01.99)	GB	9900838.5	15 January 1999 (15.01.99)	GB	9901945.7	28 January 1999 (28.01.99)	GB	9901948.1	28 January 1999 (28.01.99)	GB	9902078.6	29 January 1999 (29.01.99)	GB	9902088.5	29 January 1999 (29.01.99)	GB	9902074.5	29 January 1999 (29.01.99)	GB	9902879.7	9 February 1999 (09.02.99)	GB	9902936.5	10 February 1999 (10.02.99)	GB	9903978.6	20 February 1999 (20.02.99)	GB	9904133.7	23 February 1999 (23.02.99)	GB	9904404.2	25 February 1999 (25.02.99)	GB	<b>[BE/BE]; SmithKline Beecham Biologicals S.A., Rue de l'Institut 89, B-1330 Rixensart (BE).</b> <b>(74) Agent:</b> PRIVETT, Kathryn, Louise; SmithKline Beecham, Two New Horizons Court, Brentford, Middlesex TW8 9EP (GB). <b>(81) Designated States:</b> AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report</i>  <b>(88) Date of publication of the international search report:</b> 16 November 2000 (16.11.00)
9900952.4	15 January 1999 (15.01.99)	GB																																					
9900838.5	15 January 1999 (15.01.99)	GB																																					
9901945.7	28 January 1999 (28.01.99)	GB																																					
9901948.1	28 January 1999 (28.01.99)	GB																																					
9902078.6	29 January 1999 (29.01.99)	GB																																					
9902088.5	29 January 1999 (29.01.99)	GB																																					
9902074.5	29 January 1999 (29.01.99)	GB																																					
9902879.7	9 February 1999 (09.02.99)	GB																																					
9902936.5	10 February 1999 (10.02.99)	GB																																					
9903978.6	20 February 1999 (20.02.99)	GB																																					
9904133.7	23 February 1999 (23.02.99)	GB																																					
9904404.2	25 February 1999 (25.02.99)	GB																																					
<b>(54) Title:</b> NEISSERIA MENINGITIDIS ANTIGENIC POLYPEPTIDES, CORRESPONDING POLYNUCLEOTIDES AND PROTECTIVE ANTIBODIES <b>(57) Abstract</b> <p>The invention provides Neisseria meningitidis BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 and BASB071 polypeptides, and polynucleotides encoding BASB051, BASB057, BASB060, BASB061, BASB063, BASB065, BASB066 and BASB071 polypeptides, and methods for producing such polypeptides by recombinant techniques. Also provided are diagnostic, prophylactic and therapeutic uses thereof.</p>																																							

Docket No.: BM45348

PCT/EP00/00135

DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

NOVEL COMPOUNDS

the specification of which (check one)

- ☐ is attached hereto.
- ☒ was filed on 10 January 2000 as Serial No. PCT/EP00/00135 and was amended on (if applicable).

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the patentability as defined in Title 37, Code of Federal Regulations, Section 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, Section 119(a)-(d) or Section 365(b) of any foreign application(s) for patent or inventor's certificate, or Section 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application(s)			
Number	Country	Filing Date	Priority Claimed
9900952.4	Great Britain	15 January 1999	Yes
9900838.5	Great Britain	15 January 1999	Yes
9901945.7	Great Britain	28 January 1999	Yes
9901948.1	Great Britain	28 January 1999	Yes
9902078.6	Great Britain	29 January 1999	Yes
9902088.5	Great Britain	29 January 1999	Yes
9902074.5	Great Britain	29 January 1999	Yes
9902879.7	Great Britain	9 February 1999	Yes
9902936.5	Great Britain	10 February 1999	Yes
9903978.6	Great Britain	20 February 1999	Yes
9904133.7	Great Britain	23 February 1999	Yes
9904404.2	Great Britain	25 February 1999	Yes

I hereby claim the benefit under Title 35, United States Code, Section 119(e) of any United States provisional application(s) listed below.

Application Number      Filing Date

I hereby claim the benefit under Title 35, United States Code, Section 120 of any United States application(s) or Section 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of Title 35, United States Code, Section 112, I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application.

Serial No.      Filing Date      Status

I hereby appoint the practitioners associated with the Customer Number provided below to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith, and direct that all correspondence be addressed to that Customer Number:

Customer Number 25,308

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

1-00 Full Name of Inventor: Jean-Louis RUELLE

Inventor's Signature: [Signature] Date: 31 January 2002

Residence: Rixensart, Belgium BEX

Citizenship: Belgian

Post Office Address: SmithKline Beecham Corporation  
Corporate Intellectual Property - UW2220  
P.O. Box 1539  
King of Prussia, Pennsylvania 19406-0939

2-00 Full Name of Inventor: Joelle THONNARD

Inventor's Signature: [Signature] Date: 31.01.02

Residence: Rixensart, Belgium BEX

Citizenship: Belgian

Post Office Address: SmithKline Beecham Corporation  
Corporate Intellectual Property - UW2220  
P.O. Box 1539  
King of Prussia, Pennsylvania 19406-0939





WO 00/42191

PCT/EP00/00135

35	40	45
Ser Asn Tyr Thr Arg Ala Val Lys Leu Tyr Glu Ile Leu Glu Ser Arg		
50	55	60
Phe Pro Thr Ser Arg His Ala Arg Gln Ser Gln Leu Asp Thr Ala Tyr		
65	70	75
Ala Tyr Tyr Lys Asp Asp Glu Lys Asp Lys Ala Leu Ala Ala Ile Glu		
85	90	95
Arg Phe Arg Arg Leu His Pro Gln His Pro Asn Met Asp Tyr Ala Leu		
100	105	110
Tyr Leu Arg Gly Leu Val Leu Phe Asn Glu Asp Gln Ser Phe Leu Asn		
115	120	125
Lys Leu Ala Ser Gln Asp Trp Ser Asp Arg Asp Pro Lys Ala Asn Arg		
130	135	140
Glu Val Thr Gln Ala Phe Ala Glu Leu Val Gln Arg Phe Pro Asn Ser		
145	150	155
Lys Tyr Ala Ala Asp Ala Thr Ala Arg Met Val Lys Leu Val Asp Ala		
165	170	175
Leu Gly Gly Asn Glu Met Ser Val Ala Arg Tyr Tyr Met Lys Arg Gly		
180	185	190
Ala Tyr Ile Ala Ala Ala Asn Arg Ala Gln Lys Ile Ile Gly Ser Tyr		
195	200	205
Gln Asn Thr Arg Tyr Val Glu Glu Ser Leu Ala Ile Leu Glu Leu Ala		
210	215	220
Tyr Gln Lys Leu Gly Lys Pro Gln Leu Ala Ala Asp Thr Arg Arg Val		
225	230	235
Leu Glu Thr Asn Phe Pro Lys Ser Pro Phe Leu Thr His Ala Trp Gln		
245	250	255
Pro Asp Asp Met Pro Trp Trp Arg Tyr Trp His		
260	265	

<210> 3

<211> 1404

<212> DNA

<213> *Neisseria meningitidis*

<400> 3

atggatacta cattgaaaac caccttgact tctgttgacag cagccttcgc attatccgcc	60
tgcacatga ttccccaata cgagcagccc aaagtgcgaag ttgccgaaac gtttaaaaac	120
gataccgccc acagcggcat ccgtgcggtc gatttaggtt ggcatagacta ttttgccgac	180
ccgcgcctgc aaaagctgat cgacatcgca ctgcagcgca ataccagttt gcgtaccgcc	240
gtattgaaca gcgaaatcta ccgcaaacaac tacatgattg agcgcaacaac cctcctgccc	300
acgcttgccc ccaatgcgaa cggctcgccg caaggcagct tgagcggcgg caatgtcagc	360
agcagctaca atgtcggact ggggtcggca tcttacgaac tcgacctgtt cggacgcgtc	420
cgcagcagca gcgaagcagc actgcaaggc tatattgcaa gtgtcgccaa ccgcgatgcg	480
gcacatttga gcctgattgc caccgttgcc aaagcctatt tcaacgaacg ttatgccgaa	540
gaagcgatgt ctttgccgca gcgtgttttg aaaacgcgcg aggaaaccta caagctgtcc	600
gaattacggtt acaaggcagg cgtgatttcc gccgtcgccc tacgtcagca ggaagccctg	660

WO 00/42191

PCT/EP00/00135

```

atcgaatctg ccaaagccga ttatgcccat gccgcgcgca gccgcgaaca ggcgcgcaat    720
gccttgccaa ccttgattaa ccaaccgata cccgaagacc tgcccgccgg ttgcccgtg      780
gacaagcagt tttttgttga aaaactgccg gccggtttga gttccgaagt attgctcgac      840
cgtcccgata tccgtgctgc cgaacacgcg ctcaaacagg caaacgccaa tatcggtgcg      900
gcacgcgccg cctttttccc atccatccgc ctgaccggaa ccgtcggtac gggttctgcc      960
gaattgggtg ggttggtcaa aagcggcacg ggcgtttggc cggtcgcgcc gtctattacc    1020
ctgccgattt ttacctgggg tacgaacaaa gccaaccttg atgtagccaa gctgcgccaa    1080
caggcacaaa tcgttgcta tgaagccgcc gtccaatccg catttcaaga cgtggcaaac    1140
gcattggcgg cgcgcgagca gctggataaa gcctatgacg ctttaagcaa acaaagccgc    1200
gcctctaaag aggcgttgcg cttggtcggc ctgcgttaca agcacggcgt atccggcgcg    1260
ctcgacttgc tcgatgcgga acgcagcagc tatgcggcgg aggggtgcggc ttgtcggca    1320
caactgaccc gcgccgaaaa ccttgccgat ttgtacaagg cactcggcgg cggattgaaa    1380
cgggataccc aaaccgacaa ataa                                     1404

```

<210> 4

<211> 467

<212> PRT

<213> *Neisseria meningitidis*

<400> 4

```

Met Asp Thr Thr Leu Lys Thr Thr Leu Thr Ser Val Ala Ala Ala Phe
 1              5              10              15
Ala Leu Ser Ala Cys Thr Met Ile Pro Gln Tyr Glu Gln Pro Lys Val
      20              25              30
Glu Val Ala Glu Thr Phe Lys Asn Asp Thr Ala Asp Ser Gly Ile Arg
      35              40              45
Ala Val Asp Leu Gly Trp His Asp Tyr Phe Ala Asp Pro Arg Leu Gln
      50              55              60
Lys Leu Ile Asp Ile Ala Leu Glu Arg Asn Thr Ser Leu Arg Thr Ala
65              70              75              80
Val Leu Asn Ser Glu Ile Tyr Arg Lys Gln Tyr Met Ile Glu Arg Asn
      85              90              95
Asn Leu Leu Pro Thr Leu Ala Ala Asn Ala Asn Gly Ser Arg Gln Gly
      100             105             110
Ser Leu Ser Gly Gly Asn Val Ser Ser Ser Tyr Asn Val Gly Leu Gly
      115             120             125
Ala Ala Ser Tyr Glu Leu Asp Leu Phe Gly Arg Val Arg Ser Ser Ser
      130             135             140
Glu Ala Ala Leu Gln Gly Tyr Phe Ala Ser Val Ala Asn Arg Asp Ala
145             150             155             160
Ala His Leu Ser Leu Ile Ala Thr Val Ala Lys Ala Tyr Phe Asn Glu
      165             170             175
Arg Tyr Ala Glu Glu Ala Met Ser Leu Ala Gln Arg Val Leu Lys Thr
      180             185             190
Arg Glu Glu Thr Tyr Lys Leu Ser Glu Leu Arg Tyr Lys Ala Gly Val
      195             200             205
Ile Ser Ala Val Ala Leu Arg Gln Gln Glu Ala Leu Ile Glu Ser Ala

```

WO 00/42191

PCT/EP00/00135

```

      210              215              220
Lys Ala Asp Tyr Ala His Ala Ala Arg Ser Arg Glu Gln Ala Arg Asn
225              230              235              240
Ala Leu Ala Thr Leu Ile Asn Gln Pro Ile Pro Glu Asp Leu Pro Ala
      245              250              255
Gly Leu Pro Leu Asp Lys Gln Phe Phe Val Glu Lys Leu Pro Ala Gly
      260              265              270
Leu Ser Ser Glu Val Leu Leu Asp Arg Pro Asp Ile Arg Ala Ala Glu
      275              280              285
His Ala Leu Lys Gln Ala Asn Ala Asn Ile Gly Ala Ala Arg Ala Ala
      290              295              300
Phe Phe Pro Ser Ile Arg Leu Thr Gly Thr Val Gly Thr Gly Ser Ala
305              310              315              320
Glu Leu Gly Gly Leu Phe Lys Ser Gly Thr Gly Val Trp Ser Phe Ala
      325              330              335
Pro Ser Ile Thr Leu Pro Ile Phe Thr Trp Gly Thr Asn Lys Ala Asn
      340              345              350
Leu Asp Val Ala Lys Leu Arg Gln Gln Ala Gln Ile Val Ala Tyr Glu
      355              360              365
Ala Ala Val Gln Ser Ala Phe Gln Asp Val Ala Asn Ala Leu Ala Ala
      370              375              380
Arg Glu Gln Leu Asp Lys Ala Tyr Asp Ala Leu Ser Lys Gln Ser Arg
385              390              395              400
Ala Ser Lys Glu Ala Leu Arg Leu Val Gly Leu Arg Tyr Lys His Gly
      405              410              415
Val Ser Gly Ala Leu Asp Leu Leu Asp Ala Glu Arg Ser Ser Tyr Ala
      420              425              430
Ala Glu Gly Ala Ala Leu Ser Ala Gln Leu Thr Arg Ala Glu Asn Leu
      435              440              445
Ala Asp Leu Tyr Lys Ala Leu Gly Gly Gly Leu Lys Arg Asp Thr Gln
      450              455              460
Thr Asp Lys
465

```

<210> 5

<211> 420

<212> DNA

<213> *Neisseria meningitidis*

<400> 5

```

atgaaaaaac ttctaattgat aaccctcacc ggtatgcttg cagcttggtgc aacaggtgtc      60
aatgtcggcc gggtgatggt tgaaatgccg cagggagaac gttctgtcgt tgtgcaggtt      120
cccgcgacaa ataaccgct ttccgatacg gtagctgtcg gaatgattaa aacatccggt      180
tcgccttcgg catcaaatat gattgaaatg ctcggcgcgg acaatatcaa cgtcggcggtg      240
gtgggaagca gccaaatgct taataaggcg accgcacttt attccttaaa ccatgcaaag      300
aaagtcggaa ataattgtcag tgtttatatg atgggcgcga gcgaaagtga caaggccgat      360
ttggaaaacg cggcaaatgc caaaaatatc aaattgcatt atttctttta ccaaaaataa      420

```





WO 00/42191

PCT/EP00/00135

<212> PRT

<213> *Neisseria meningitidis*

<400> 10

```

Met Arg Pro Tyr Ala Thr Thr Ile Tyr Gln Leu Phe Ile Leu Phe Ile
 1           5           10           15
Gly Ser Val Phe Thr Met Thr Ser Cys Glu Pro Val Asn Glu Lys Thr
          20           25           30
Asp Gln Lys Ala Val Ser Ala Gln Gln Ala Lys Glu Gln Thr Ser Phe
          35           40           45
Asn Asn Pro Glu Pro Met Thr Gly Phe Glu His Thr Val Thr Phe Asp
          50           55           60
Phe Gln Gly Thr Lys Met Val Ile Pro Tyr Gly Tyr Leu Ala Arg Tyr
65           70           75           80
Thr Gln Asp Asn Ala Thr Lys Trp Leu Ser Asp Thr Pro Gly Gln Asp
          85           90           95
Ala Tyr Ser Ile Asn Leu Ile Glu Ile Ser Val Tyr Tyr Lys Lys Thr
          100          105          110
Asp Gln Gly Trp Val Leu Glu Pro Tyr Asn Gln Gln Asn Lys Ala His
          115          120          125
Phe Ile Gln Phe Leu Arg Asp Gly Leu Asp Ser Val Asp Asp Ile Val
          130          135          140
Ile Arg Lys Asp Ala Cys Ser Leu Ser Thr Thr Met Gly Glu Arg Leu
          145          150          155          160
Leu Thr Tyr Gly Val Lys Lys Met Pro Ser Ala Tyr Pro Glu Tyr Glu
          165          170          175
Ala Tyr Glu Asp Lys Arg His Ile Pro Glu Asn Pro Tyr Phe His Glu
          180          185          190
Phe Tyr Tyr Ile Lys Lys Gly Glu Asn Pro Ala Ile Ile Thr His Arg
          195          200          205
Asn Asn Arg Ile Asn Gln Thr Glu Glu Asp Ser Tyr Ser Thr Ser Val
          210          215          220
Gly Ser Cys Ile Asn Gly Phe Thr Val Gln Tyr Tyr Pro Phe Ile Arg
          225          230          235          240
Glu Lys Gln Gln Leu Thr Gln Gln Glu Leu Val Gly Tyr His Gln Gln
          245          250          255
Val Glu Gln Leu Val Gln Ser Phe Val Asn Asn Ser Asn Lys Lys
          260          265          270

```

<210> 11

<211> 717

<212> DNA

<213> *Neisseria meningitidis*

<400> 11

```

atgaagacca aattaccgct ttttatcatt tggctgtccg tatccgccgc ctgttcttcc      60
cctgtttccc gcaatattca ggatatgcgg cccgaaccgc aggcagaggc aggtagtctg      120

```

WO 00/42191

PCT/EP00/00135

```

gacgctattc cctatcccggt tcccactctg caagaccggtt tggattatct ggaaggcaca      180
ctcgtccgcc tgtcgaacga agtggaaacc ttaaaccggca aagtcaaagc actggagcat      240
gcgaaaaacac acccttccgg tagggcatac gtccaaaaaac tcgacgaccg caagttgaaa      300
gagcattacc tcaataccga aggcggcagc gcatccgcac ataccgtcga aaccgcacaa      360
aacctctaca atcaggcact caaacactat aaaagcggca ggttttctgc cgcagccgcc      420
ctggttgaag gcgcggacgg aggcgacggc ggcagcatcg cgcaacgcag tatgtacctg      480
ttgctgcaaa gcagggcgcg tatgggcaac tgcgaatccg tcatcgaaat cggagggcgt      540
tacgccaaacc gtttcaaaga cagccaacc gcgccgaag ccatgttcaa aatcggcgaa      600
tgccaataca ggttgacga gaaagacatt gcaagggcaa cttggcgag cctgatacag      660
gcttaccgga gcagcccgcc ggcaaacgc gccgccgag ccgtacgcaa acgatatg      717

```

<210> 12

<211> 238

<212> PRT

<213> *Neisseria meningitidis*

<400> 12

```

Met Lys Thr Lys Leu Pro Leu Phe Ile Ile Trp Leu Ser Val Ser Ala
 1             5             10             15
Ala Cys Ser Ser Pro Val Ser Arg Asn Ile Gln Asp Met Arg Pro Glu
      20             25             30
Pro Gln Ala Glu Ala Gly Ser Ser Asp Ala Ile Pro Tyr Pro Val Pro
      35             40             45
Thr Leu Gln Asp Arg Leu Asp Tyr Leu Glu Gly Thr Leu Val Arg Leu
      50             55             60
Ser Asn Glu Val Glu Thr Leu Asn Gly Lys Val Lys Ala Leu Glu His
      65             70             75             80
Ala Lys Thr His Pro Ser Gly Arg Ala Tyr Val Gln Lys Leu Asp Asp
      85             90             95
Arg Lys Leu Lys Glu His Tyr Leu Asn Thr Glu Gly Gly Ser Ala Ser
      100            105            110
Ala His Thr Val Glu Thr Ala Gln Asn Leu Tyr Asn Gln Ala Leu Lys
      115            120            125
His Tyr Lys Ser Gly Arg Phe Ser Ala Ala Ala Leu Leu Lys Gly
      130            135            140
Ala Asp Gly Gly Asp Gly Gly Ser Ile Ala Gln Arg Ser Met Tyr Leu
      145            150            155            160
Leu Leu Gln Ser Arg Ala Arg Met Gly Asn Cys Glu Ser Val Ile Glu
      165            170            175
Ile Gly Gly Arg Tyr Ala Asn Arg Phe Lys Asp Ser Pro Thr Ala Pro
      180            185            190
Glu Ala Met Phe Lys Ile Gly Glu Cys Gln Tyr Arg Leu Gln Gln Lys
      195            200            205
Asp Ile Ala Arg Ala Thr Trp Arg Ser Leu Ile Gln Ala Tyr Pro Ser
      210            215            220
Ser Pro Ala Ala Lys Arg Ala Ala Ala Val Arg Lys Arg
      225            230            235

```

WO 00/42191

PCT/EP00/00135

<210> 13  
<211> 1176  
<212> DNA  
<213> *Neisseria meningitidis*

<400> 13  
gtgtttaaag tgaaatttta tattcgtcac gcagttattat tattgtgtgg aagtttaatt 60  
gtaggatgct ctgcgattcc ttcatacaggc cccagcgcaa aaaaaattgt ctcttttaggg 120  
caacaatctg aagttcaaat tcctgaagtg gagctgattg atgtgaatca tacgggttgct 180  
cagttattat ataaggctca gataaatcag tcattcactc agtttggcga tggttatgct 240  
tcggctggta cgctaaatat tggatgata ttggatatta tgatttggga agcgccgccg 300  
gcagttattgt ttggtggtgg cctttcttcg atgggctcgg gtagtgcgca tcaaactaag 360  
ttgccagagc agttggtcac ggcacgtggt acggtttctg tgccgtttgt tggcgatatt 420  
tcgggtggtc gtaaaacgcc tggtcaggtt caggaaatta ttaaaggccg cctgaaaaaa 480  
atggccaatc agccacaagt gatggtgcgt ttggtgcaga ataatgcggc gaatgtgtcg 540  
gtgattcgtg ctgggaatat tgtgcgtatg ccgctgacgg cagccggtga gcgtgtgttg 600  
gatgcggtgg ctgcggtagg tggttcaacg gcaaattgtc aggatacgaa tgtgcagctg 660  
acacgtggca atgtagtacg aactgttgcc ttggaagatt tagttgcaaa tccgcgacaa 720  
aatattttgc tgcgtcgcgg tgatgtggtt accatgatta ccaatcccta tacctttacg 780  
tctatgggtg cgggtggggag aacacaagaa atcggttttt cagccagagg cttatcgctt 840  
tctgaagcca ttggccgtat gggcggtttg caagatcgcc gttctgatgc gcgtggtgtg 900  
tttgtgttcc gctatacgcc attggtggaa ttgccggcag aacgtcagga taaatggatt 960  
gctcaagggt atggcagtga ggcagagatt ccaacggtat atcgtgtgaa tatggctgat 1020  
gcgcattcgc tattttctat gcagcgctt cctgtgaaga ataaagatgt attgtatgtg 1080  
tcgaatgcgc cgttggctga agtgcagaaa ttcttgtcgt ttgtgttctc gccggttacc 1140  
agtggcgcca acagtattaa taatttaact aattaa 1176

<210> 14  
<211> 391  
<212> PRT  
<213> *Neisseria meningitidis*

<400> 14  
Met Phe Lys Val Lys Phe Tyr Ile Arg His Ala Val Leu Leu Leu Cys  
1 5 10 15  
Gly Ser Leu Ile Val Gly Cys Ser Ala Ile Pro Ser Ser Gly Pro Ser  
20 25 30  
Ala Lys Lys Ile Val Ser Leu Gly Gln Gln Ser Glu Val Gln Ile Pro  
35 40 45  
Glu Val Glu Leu Ile Asp Val Asn His Thr Val Ala Gln Leu Leu Tyr  
50 55 60  
Lys Ala Gln Ile Asn Gln Ser Phe Thr Gln Phe Gly Asp Gly Tyr Ala  
65 70 75 80  
Ser Ala Gly Thr Leu Asn Ile Gly Asp Val Leu Asp Ile Met Ile Trp  
85 90 95  
Glu Ala Pro Pro Ala Val Leu Phe Gly Gly Leu Ser Ser Met Gly





WO 00/42191

PCT/EP00/00135

```

yyccccgatg tggatttgat gaacgcgatg gcgaaggcgg gcaatttta aatcgaattc      240
aaacaccagc cgtgggacag ccttttcccc gccttgaaca acggcgatgc ggacgttggtg      300
atgtcgggcg taaccattac cgacgaccgc aaacagtcta tggacttcag cgacccttat      360
tttgaaatca cccaagtcgt cctcgttccg aaaggcaaaa aaatatcttc ttccgaagat      420
ttgaaaaaca tgaacaaagt cggcgtggta accggctaca cgggcgattt ctccgtatcc      480
aaactcttgg gcaacgacaa cccgaaaatc gcgcgctttg aaaacgttcc cctgattatc      540
aaagaactgg aaaacggcgg cttggattcc gtggtcagcg acagcgcagt catcgccaat      600
tatgtgaaaa acaatccgac caaagggatg gacttcgtta ccctgcccg cttcaccacc      660
gaacactacg gcatcgcggt acgcaaaggc gacgaagcaa ccgtcaaaaat gctgaacgat      720
gcgttgaaaa aagtacgcga aagcggcgaa tacgacaaaa tctacgcaa atattttgca      780
aaagaagacg gacaggccgc aaaataa                                           807

```

<210> 16

<211> 268

<212> PRT

<213> *Neisseria meningitidis*

<400> 16

```

Met Asn Met Lys Lys Trp Ile Ala Ala Ala Leu Ala Cys Ser Ala Leu
  1              5              10              15
Ala Leu Ser Ala Cys Gly Gly Gln Gly Lys Asp Ala Ala Ala Pro Ala
      20              25              30
Ala Asn Pro Asp Lys Val Tyr Arg Val Ala Ser Asn Ala Glu Phe Ala
      35              40              45
Pro Phe Glu Ser Leu Asp Ser Lys Gly Asn Val Glu Gly Phe Asp Val
      50              55              60
Asp Leu Met Asn Ala Met Ala Lys Ala Gly Asn Phe Lys Ile Glu Phe
      65              70              75              80
Lys His Gln Pro Trp Asp Ser Leu Phe Pro Ala Leu Asn Asn Gly Asp
      85              90              95
Ala Asp Val Val Met Ser Gly Val Thr Ile Thr Asp Asp Arg Lys Gln
      100             105             110
Ser Met Asp Phe Ser Asp Pro Tyr Phe Glu Ile Thr Gln Val Val Leu
      115             120             125
Val Pro Lys Gly Lys Lys Ile Ser Ser Ser Glu Asp Leu Lys Asn Met
      130             135             140
Asn Lys Val Gly Val Val Thr Gly Tyr Thr Gly Asp Phe Ser Val Ser
      145             150             155             160
Lys Leu Leu Gly Asn Asp Asn Pro Lys Ile Ala Arg Phe Glu Asn Val
      165             170             175
Pro Leu Ile Ile Lys Glu Leu Glu Asn Gly Gly Leu Asp Ser Val Val
      180             185             190
Ser Asp Ser Ala Val Ile Ala Asn Tyr Val Lys Asn Asn Pro Thr Lys
      195             200             205
Gly Met Asp Phe Val Thr Leu Pro Asp Phe Thr Thr Glu His Tyr Gly
      210             215             220
Ile Ala Val Arg Lys Gly Asp Glu Ala Thr Val Lys Met Leu Asn Asp

```

[illegible]

**WO 00/42191**

**PCT/EP00/00135**

225                      230                      235                      240  
Ala Leu Lys Lys Val Arg Glu Ser Gly Glu Tyr Asp Lys Ile Tyr Ala  
                        245                      250                      255  
Lys Tyr Phe Ala Lys Glu Asp Gly Gln Ala Ala Lys  
                        260                      265